

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2000, 05:58:36 ; Search time 17336.7 Seconds  
(without alignments)  
-3281.814 Million cell updates/sec

Title: US-09-339-352-9  
Perfect score: 18738  
Sequence: 1 aaataacaatttagttgc.....gagcctcatatcgtgac 18738

Scoring table: IDENTIFY\_NTC

Searched: 82193 seqs, -1518192014 residues

Database: GenEmbl.\*

Word size: 0

Number of hits that pass the threshold: 1642386

1: gb\_bal:\*  
2: gb\_bal:\*  
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45: gb\_bal:\*  
46: gb\_bal:\*  
47: gb\_bal:\*  
48: gb\_bal:\*  
49: gb\_bal:\*

50: gb\_pl3:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18738	100.0	102258	11	HS295C6	297876 Human DNA s
2	1427.4	7.6	184421	42	AC012066	AC012066 Homo sapi
3	1351.4	7.1	223542	40	AC006515	AC006515 Homo sapi
4	1262.4	6.7	126766	11	HSJ15413	AL049574 Human DNA
5	1242.8	6.6	137111	10	HS20723	AL022576 Human DNA
6	1242.4	6.6	81746	41	AC011408	AL011408 Homo sapi
7	1235.6	6.6	92171	40	AC004924	AC004924 Homo sapi
8	1226	6.5	152077	10	HS13062	AL008627 Human DNA
9	1222.8	6.5	104594	11	HSJ09014	AL049550 Human DNA
10	1207.4	6.4	134187	40	AC004704	AC004704 Homo sapi
11	1201.2	6.4	94220	41	AC008886	AC008886 Homo sapi
12	1200.6	6.4	165491	11	AC000385	AC000385 Human Chr
13	1199	6.4	35281	11	HS196A2	268165 Human DNA s
14	1183.4	6.3	58645	11	AC002068	AC002068 Homo sapi
15	1175	6.3	171212	41	AC009408	AC009408 Homo sapi
16	1165.8	6.2	179757	40	AC006960	AC006960 Homo sapi
17	1165.6	6.2	140338	43	AC011686	AL011686 Homo sapi
18	1164.4	6.2	150871	32	HSJ18774	AL109808 Homo sapi
19	1158.2	6.2	171377	10	CNS01DSX	AL122023 Human chr
20	1154.8	6.2	119427	32	AP000560	AP000560 Homo sapi
21	1146	6.1	155661	11	HS399M14	296074 Human DNA s
22	1145	6.1	98778	32	AC002408	AC002408 Homo sapi
23	1135.4	6.1	176257	44	AC006039	AC006039 Homo sapi
24	1125.8	6.0	182374	44	AC008114	AC008114 Homo sapi
25	1124.2	6.0	297111	42	AC007545	AC007545 Homo sapi
26	1116.2	6.0	93481	40	AF201337	AF201337 Homo sapi
27	1111.6	5.9	169340	40	AC009248	AC009248 Homo sapi
28	1099.4	5.9	215788	40	AC007308	AC007308 Homo sapi
29	1098.6	5.9	154269	41	AC011350	AC011350 Homo sapi
30	1095.2	5.8	41935	11	HSU61B11	273913 Human DNA s
31	1093.8	5.8	211134	40	AC008009	AC008009 Homo sapi
32	1092.6	5.8	133072	10	HS1097P24	AL035258 Human DNA
33	1091.4	5.8	128330	10	HS111D6	AL031056 Human DNA
34	1090.4	5.8	247661	43	AC012154	AC012154 Homo sapi
35	1090.2	5.8	235395	40	AC002470	AC002470 Homo sapi
36	1089.6	5.8	130705	10	HS232L22	273986 Human DNA s
37	1089.6	5.8	39876	11	HSU83C4	270050 Human DNA s
38	1088.6	5.8	105933	33	AC005407	AC005407 Homo sapi
39	1088.6	5.8	108487	11	HS738P15	AL035252 Human DNA
40	1085	5.8	204412	33	HSJ1025A1	AL080312 Homo sapi
41	1083.4	5.8	210680	44	AC013530	AC013530 Homo sapi
42	1081	5.8	177483	11	HSJ148M19	AL050309 Human DNA
43	1078.8	5.8	66817	11	AC005201	AC005201 Homo sapi
44	1072.4	5.7	166182	33	CNS01DUE	AL133241 Homo sapi
45	1072.4	5.7	184659	44	AC016708	AC016708 Homo sapi

# ALIGNMENTS

RESULT 1  
HS295C6 102258 bp DNA PRI 23-NOV-1999  
LOCUS Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains  
DEFINITION ESTs, CA repeat, STRs and Cpg island.  
ACCESSION 297876  
VERSION 1q24; Cpg island; repeat polymorphism.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 102258)  
AUTHORS Grafham,D.  
TITLE Direct Submission  
JOURNAL Submitted (27-Oct-1997) Chromosome 1 Project Group, Hinxton,  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Nov 2, 1997 this sequence version replaced g1:2465042.  
COMMENT IMPORTANT: This sequence is the entire insert of clone 295C6.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variations annotated may not be found in the sequence submission  
corresponding to the overlapping clone as we submit sequences with  
only a small overlap as described above.  
This sequence was generated from part of bacterial clone contigs of  
human chromosome 1, constructed by the Sanger Centre chromosome 1  
mapping group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1/  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The true left end of clone 295C6 is at 1 in this sequence. The true  
right end of clone 295C6 is at 102258.  
295C6 is from the library RPCII constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong.  
For further details see http://bacpac.med.buffalo.edu/.  
FEATURES  
source 1.102258  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/map="1q24"  
/clone="RP1-295C6"  
/clone\_1kb="RPC1-1"  
891..1180  
repeat\_region repeat: matches 298. .9 of consensus"  
/note="Alusg repeat: matches 298. .9 of consensus"  
1375..1683  
repeat\_region repeat: matches 303. .1 of consensus"  
/note="Alusp repeat: matches 303. .1 of consensus"  
2028..2310  
repeat\_region repeat: matches 300. .1 of consensus"  
/note="Alusg repeat: matches 300. .1 of consensus"  
2612..2903  
repeat\_region repeat: matches 301. .1 of consensus"  
/note="Alusx repeat: matches 301. .1 of consensus"  
complement(4475..4866)  
/note="match: 223618 STS containing (CA) repeat"  
4625..4670  
repeat\_region repeat: matches 146. .60 of consensus"  
/note="23 copies of GT 100 & conserved; differs from  
223618"  
4766..4897  
repeat\_region repeat: matches 145. .1 of consensus"  
/note="MIR2 repeat: matches 145. .1 of consensus"  
4969..5140  
repeat\_region repeat: matches 1475. .1300 of consensus"  
/note="MER42c repeat: matches 1475. .1300 of consensus"  
5146..5448  
repeat\_region repeat: matches 302. .1 of consensus"  
/note="Alufo repeat: matches 302. .1 of consensus"  
5503..5795  
repeat\_region repeat: matches 1. .299 of consensus"  
/note="Alusg repeat: matches 1. .299 of consensus"  
5797..5925  
repeat\_region repeat: matches 1265. .1124 of consensus"  
/note="MER42c repeat: matches 1265. .1124 of consensus"  
5923..6039  
repeat\_region repeat: matches 920. .804 of consensus"  
/note="L1MB6 repeat: matches 920. .804 of consensus"  
6123..6415  
repeat\_region repeat: matches 1. .292 of consensus"  
/note="Alusx repeat: matches 1. .292 of consensus"  
7799..8099  
repeat\_region repeat: matches 302. .1 of consensus"  
/note="Alusx repeat: matches 302. .1 of consensus"  
9002..9302  
repeat\_region repeat: matches 2. .303 of consensus"  
/note="Alusp repeat: matches 2. .303 of consensus"  
9692..9983  
repeat\_region repeat: matches 1. .301 of consensus"  
/note="Alufo repeat: matches 1. .301 of consensus"  
10986..11071  
repeat\_region repeat: matches 146. .60 of consensus"  
/note="MIR2 repeat: matches 146. .60 of consensus"

repeat\_region 11583..11766  
/note="MIR repeat: matches 262. .70 of consensus"  
repeat\_region 12180..12479  
/note="Alusg repeat: matches 1. .300 of consensus"  
13246..13500  
repeat\_region repeat: matches 256. .1 of consensus"  
/note="MIR repeat: matches 256. .1 of consensus"  
13907..13973  
repeat\_region repeat: matches 75. .141 of consensus"  
/note="MIR repeat: matches 75. .141 of consensus"  
13975..14489  
repeat\_region repeat: matches 526. .1 of consensus"  
/note="MER1A repeat: matches 526. .1 of consensus"  
15702..16064  
repeat\_region repeat: matches 1. .371 of consensus"  
/note="RHEIC repeat: matches 1. .371 of consensus"  
16144..16585  
repeat\_region repeat: matches 9. .466 of consensus"  
/note="MTRIC repeat: matches 9. .466 of consensus"  
17173..17534  
repeat\_region repeat: matches 105. .449 of consensus"  
/note="LRR2 repeat: matches 105. .449 of consensus"  
417786..418427  
/note="match: multiple ESTs; match: AA165668 C16515  
AA077391"  
18004..18120  
repeat\_region repeat: matches 39 mer 81 & conserved"  
/note="3 copies of 39 mer 81 & conserved"  
19377..>21532  
prim\_transcript prim\_transcript match: N46036 H60052 H12822  
/note="match: multiple ESTs; match: T57635 F00049 N75628 AA382351  
T62974 AA283144; match: W37181 N52820 AA337499 W87891 H84729;  
AA300207; match: W37181 N52820 AA337499 W87891 H84729;  
similar to endogenous retrovirus POL POLYPROTEIN"  
422156..22928  
prim\_transcript prim\_transcript match: AA401243 AA258918  
/note="match: multiple ESTs; match: AA401243 AA258918  
AA248892 AA096209 R36280"  
23025..23060  
repeat\_region repeat: matches 12 mer 94 & conserved"  
/note="3 copies of 12 mer 94 & conserved"  
23519..23865  
repeat\_region repeat: matches 105. .449 of consensus"  
/note="LRR2 repeat: matches 105. .449 of consensus"  
24473..24785  
repeat\_region repeat: matches 1. .299 of consensus"  
/note="Alusg repeat: matches 1. .299 of consensus"  
25027..25058  
repeat\_region repeat: matches 16 copies of 2 mer 88 & conserved"  
/note="16 copies of 2 mer 88 & conserved"  
25877..25987  
repeat\_region repeat: matches 788. .892 of consensus"  
/note="L1PA5 repeat: matches 788. .892 of consensus"  
26022..26312  
repeat\_region repeat: matches 1. .295 of consensus"  
/note="Alusp repeat: matches 1. .295 of consensus"  
26752..27050  
repeat\_region repeat: matches 1. .299 of consensus"  
/note="Alusg repeat: matches 1. .299 of consensus"  
28012..28312  
repeat\_region repeat: matches 1. .303 of consensus"  
/note="Alusg repeat: matches 1. .303 of consensus"  
28316..29086  
repeat\_region repeat: matches 109. .907 of consensus"  
/note="L1ME3A repeat: matches 109. .907 of consensus"  
29517..29629  
repeat\_region repeat: matches 262. .151 of consensus"  
/note="MIR repeat: matches 262. .151 of consensus"  
29631..29928  
repeat\_region repeat: matches 1. .295 of consensus"  
/note="Alu repeat: matches 1. .295 of consensus"  
29937..30237  
repeat\_region repeat: matches 1. .301 of consensus"  
/note="Alusg repeat: matches 1. .301 of consensus"  
30238..30315  
repeat\_region repeat: matches 158. .76 of consensus"  
/note="MIR repeat: matches 158. .76 of consensus"  
31096..31287  
repeat\_region repeat: matches 56. .262 of consensus"  
/note="MIR repeat: matches 56. .262 of consensus"  
31289..31379  
repeat\_region repeat: matches 146. .56 of consensus"  
/note="MIR2 repeat: matches 146. .56 of consensus"  
31479..31525  
repeat\_region repeat: matches 146. .95 of consensus"  
/note="MIR2 repeat: matches 146. .95 of consensus"  
33069..33318  
repeat\_region repeat: matches 262. .74 of consensus"  
/note="MIR repeat: matches 262. .74 of consensus"  
35565..35744  
repeat\_region repeat: matches 1. .302 of consensus"  
/note="Alusx repeat: matches 1. .302 of consensus"  
36165..36466  
repeat\_region repeat: matches 1. .302 of consensus"  
/note="Alusx repeat: matches 1. .302 of consensus"  
36992..36944  
repeat\_region repeat: matches 3. .240 of consensus"  
/note="MIR repeat: matches 3. .240 of consensus"  
36999..37299  
repeat\_region repeat: matches 301. .1 of consensus"  
/note="Alusx repeat: matches 301. .1 of consensus"  
37924..38114  
repeat\_region repeat: matches 1055. .866 of consensus"  
/note="L1MA2 repeat: matches 1055. .866 of consensus"

repeat\_region 38108..38475  
/note="MIRA repeat: matches 425..1 of consensus"  
repeat\_region 38479..38657  
/note="LIM2 repeat: matches 874..687 of consensus"  
repeat\_region 38658..38957  
/note="AlusB repeat: matches 300..1 of consensus"  
repeat\_region 38958..39580  
/note="LIM3 repeat: matches 699..85 of consensus"  
repeat\_region 39585..39875  
/note="AlusG repeat: matches 292..1 of consensus"  
repeat\_region 39877..39951  
/note="LIM9 repeat: matches 88..14 of consensus"  
repeat\_region 39944..40919  
/note="L1 repeat: matches 4416..5390 of consensus"  
repeat\_region 40769..41862  
/note="L1Pa2 repeat: matches 1..893 of consensus"  
repeat\_region 41764..42556  
/note="L1 repeat: matches 5133..4305 of consensus"  
repeat\_region 42557..42857  
/note="AluY repeat: matches 1..301 of consensus"  
repeat\_region 42876..43925  
/note="L1 repeat: matches 4313..3215 of consensus"  
repeat\_region 44235..44498  
/note="MER43 repeat: matches 3..272 of consensus"  
repeat\_region 44788..44860  
/note="MIR repeat: matches 154..82 of consensus"  
repeat\_region 44933..45220  
/note="AlusG repeat: matches 289..2 of consensus"  
unSURE 45304..45336  
/note="AluY repeat: matches 1..301 of consensus"  
repeat\_region 45337..45637  
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repeat\_region 45934..46220  
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repeat\_region 46817..46935  
/note="MIR repeat: matches 35..154 of consensus"  
repeat\_region 47393..47677  
/note="AlusB repeat: matches 1..302 of consensus"  
repeat\_region 48309..48404  
/note="MIR repeat: matches 48..140 of consensus"  
repeat\_region 48620..48862  
/note="MER21B repeat: matches 347..102 of consensus"  
repeat\_region 48865..49159  
/note="AlusC repeat: matches 1..296 of consensus"  
repeat\_region 51182..51467

Query Match 100.0%; Score 18738; DB 11; Length 102258;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 18738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aataaacaatttggctgccttgaaattcaatgaacctataataaactgaataaact 60  
DB 83521 AATTAATAAATTAAGTGGCTTGAACTTCAATGAACCTTAATAATAAATGACATAAAT 83580  
QY 61 tactccaatttccttatgagagaattactgttaataaatatataagaatccta 120  
DB 83581 TACTTCCTTAATTTCTTTTGAGAGAAATTAATCTTAATAAATTAATTAATGAATCCGA 83640  
QY 121 ccagaagaatgagccactatcgtatatagaattccctccctaagtaagaactctt 180  
DB 83641 CCCAGAAGTAGGCCACTATGATATATGATTCCTCCCTCCCAAGTAAGAAAGTAATCTTT 83700  
QY 181 tggagaagaatagtaatttttaactctcaagcacatatacacacttaacaatactgatt 240  
DB 83701 TGGAAACAGAAATAGTAATTTTACTCTCAAGCACATATACACACTTACAAATACTGGATT 83760  
QY 241 gagagatcactatctcctcgttaaaaaataaatttcttctaataagctagaaggtca 300  
DB 83761 GAGGATTCACCTATATCCCTCTGTGAAAAATTAAGTTCTTACTGAATGCTTAAGAGGTCA 83820  
QY 301 taaatacactaatctcctactcctccatcccttcatatgacactccttatagtttg 360  
DB 83821 TAAATTCATCATTTCCCTACCTCTTCCGATCCCTTTTCAATGACACTCCTTTATGTTTG 83880

QY 361 ttacttttaacacccctcttaattcccttaacttaacaaagtacacccgttgcatacat 420  
DB 83881 TTACTTTTTTAACACCCCTCTTAATTCCTTACTACATACAAAGTTCACTGTTTGCTATCAT 83940  
QY 421 gtgacaactatagatacaaatcccttagaatatgtaaggttaactctcttgacatgatactg 480  
DB 83941 GTGACAACTAGATACAAATCCTTAGAATATGTAAGGTAACTTTGACATGATGATACG 84000  
QY 481 acggccaaaataatcattcaattttatcttggtccaaagctagttctgatttaacactaga 540  
DB 84001 ACGGCCAAAATAATCATTTCTTTATTTGTCGCAAAAGTAGTTGATTTAACAATAAGA 84060  
QY 541 aactactaagctacatttttagagccatataatttaattttccacaatgacctgga 600  
DB 84061 ACATGACTTAAGCTACATTTTATGAGCCATATATTTATTTATTTTCACAAATGCTTGA 84120  
QY 601 aataactatcaataaataatagtaaccacaaacatcataggttagataaagtctttaaaatgt 660  
DB 84121 AATAGCTATCACTAATAATATAGTACCAAAACATCATGGGTAGATATGTTTTAAAAATGT 84180  
QY 661 tgactgaaataactcttggtttggaatccagagttaagaacaggttaagaactaaa 720  
DB 84181 TGACTGAAATATCACTTTGCTTGAATTCAGAGTAAAGAACAGCTAAAGAGACTAAA 84240  
QY 721 tagctaaagtatgtaggagatgataagtttaattactattctcttcaggtacaa 780  
DB 84241 TAGCTTAGATGCTATTTGTAGGGATGATAGCTTTAAATTTACTTATTTCTTCAGGTACAA 84300  
QY 781 gaatcagttacttttagatttagaagaagctgtgaatcatcatctgtaggactcataa 840  
DB 84301 GAATCAGTTACTTTTAGATTTTGAAGAAAGCTGTGAATCATCTACTGTAGGACTCATTA 84360  
QY 841 atcaggcaaatgagggccagtaaacaaattactgttttaaaataataatccacaagga 900  
DB 84361 ATCAGGCAAAATGAGGCCAGTAAACAAATTAATCTTTTAAATAATATCAACAAAGGA 84420  
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DB 84421 TAAAAAATAGTATCCCTTAATCTTAATCTTAACATATATTTATGCTTTCCCAATGAAA 84480  
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DB 84481 TCTGAGTTTCCGTAAGGTTCTGTAATGTAAAGAAAGTCTTAAGAGATACCAATATATGA 84540  
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DB 84601 GATGAGCACTTACAGATTAAATTTGTCTTAACACTGAGAGAGTTCTGGATTAGAGA 84660  
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DB 84661 ACGACTTAGACACAGATTTCTTGATCTAGTCCTGCTTTCTACTGTACATACAGACATTT 84720  
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DB 84721 AAACATATTCTCATCTCTGTTTAAGCAAAATTAATTTTACATGACCTGGAATGAT 84780  
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DB 84781 AAACATATTATAGCTTAGGGCTTTCTTCTCTTGACACATCTGATTAACAGTTCTAAT 84840  
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DB 84841 TTCTTAAAGTTTAGTTTAAAGCAGATAGCACACAAAAAATATGTAAAGTGTGACAAAC 84900  
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DB 84901 TGCAATCAAGAGATTAATCTGCTGTGTTGCCAGGCTGATTTGAATGAGAGGACGATC 84960  
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|||||  
Db 84961 TTGGCTACTGCAACCTCCATCTTCTGGTTCAAGCAATTCTCTGGCTCACCTCCAGA 85020  
QY 1501 gtatgctgggaattacaaggtgtagcaaccatgcccagcctaatttcglatittagtagag 1560  
Db 85021 GTAGCTGGATTAACAGGTGTGCACACCACTAGCCAGCTAAATTCGTATTTTGTAGAG 85080  
QY 1561 aacgggtatcaccaatgttggccagagctggtctggaactcctgattcaagtgataccacac 1620  
Db 85081 ACAAGGATACCAATGTGGCCAGGTGTCTCGAACTCTGATTTTCAAGGATCCACAC 85140  
QY 1621 gccctggcccccacaagtgctgggattacaggtgtagctacccggccagctgatactc 1680  
Db 85141 GCGTCGGCCCTCCAAAGTGTGGGATTAACAGGTGTGAGCTACCGCGCCAGCTGATATTC 85200  
QY 1681 cttttatgaaattccttcggaatacaaaactcgtgtgggtgggttcgttatttc 1740  
Db 85201 CTTTATTAATTAATCTTCTGGAATTAACAACCTGTGTGGGGGTTTCGTTATTTATCC 85260  
QY 1741 actgcttatccctgagtgccagaaacagtgcttaataatacaataagccctcataaatact 1800  
Db 85261 ACAGCTTATCCGTAGTGCAGAACAGTGTCTAATATACATTAAGCCCTCAATAAATAT 85320  
QY 1801 gaabaatcaaaccttccttggtagctgtagtggagaatattcatttcaaccaatatt 1860  
Db 85321 GAATTAATCAACCTTCTTGGTAGCTGATGTGTGAATATTTCTATTTTTCACCAATAT 85380  
QY 1861 ttacaatgatttgaattcaattcaatccttaactatttagttacttacttaacttaaat 1920  
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QY 2701 atcaattataattataaattalatagaattactgcaataataatatttgtaatacag 2760  
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Db 87481 AATCTCAAAATCTAGAAATCAGCAATGTATTTCCAACTGTAAATATGTAGCATTTTC 87540  
QY 4021 atatcatttaataacctctgttagtggaatctagaanaaatggttccaatgacattcaat 4080  
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Dh	89341	CAATTCCGAAGAAGAAAGAAATGAGTCTTTTCATGTGGTGGCCCAAGACACTTTGGTGGCCG	894000
Qy	5881	cagaagcttgagaagcctcaatctcagagatcaggttttgggttgagctcgttcgtaaggga	5940
Dh	89401	CAGAAGTTGAGAAGGCTCAAAATCTGGAGATCAGTTTGGGTTGGATGCTCGCTAAGGA	894600
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Qy	6001	gttcgagagaagaagggttgaaatgcacagcctagagagatagacggtcttaacttgaaggga	6060
Dh	89521	GTTTCAGAGAGAAAGGTTGAATATGCACAGGCTTAGAGAGATAGACGGCTTCACTTGAAGGA	895800
Qy	6061	agggaatcgaggtctgtgatatcctctaagagcaagtgtcagaagggccttaaaagttcat	6120
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Dh	89641	TTTAGAGAGAGGAGAGAAAGGCTCTCGATTAAGAGCCATTAGAGGTTCCATTAACTGCTG	897000
Qy	6181	gattgtctgtacaaacggtcctcaattctcggcgagatcagatcctcaattatcgaagagcc	6240
Dh	89701	GATGGTTGTACAAACGGCCTCAATTTCTCGGGAGCATCAGCTCCACTTATGAGAGGCC	897600
Qy	6241	ggtgtgattgtggtccgcgcaagctctcgggcacccggcgcgacatcgcgcgcggaggatcgt	6300
Dh	89761	GGTGTGATGATGGCCCGCAGGCTCTGGGACACGGGGCCCAACATCGCGCGAGGATCT	898200
Qy	6301	tggcaagccgggttggagagcgtgtgctgtctcgtcccttgctgacaaagaaaggagacta	6360
Dh	89821	TGGCAAGCCGGGTGGAGAGCTGGCTGTGTTCTGTGCTCGCTGACACGAAGGAGACTA	898800
Qy	6361	gtcaactttctctgcacagacgaactcgcgtccgcctctcgttgagttacccctcccggt	6420
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Qy	6421	ctttccctccgcgcgttgaaccgaaagcttgcgcccgcccgcccggaaggttgaagggt	6480
Dh	89941	CTTTCCCTCCCGCTGTGAAACGAAAGCTGGGGCCCGGCCCCGGAAAGTTGAGGGGG	900000
Qy	6481	cggagagctgcgcgacttgcacagccccggtccgcctccggcccccgccgaagagagggag	6540
Dh	90001	CGGAGGCTCGACATGCGACGCCCCGCGTCCGCTCCGGCCCCCGGAGAGAGAGGAGG	900600
Qy	6541	agccatgtgcacaagtggtccaataatactcaactcaaccaagtctgcgtgcgcctctgtgc	6600
Dh	90061	AGCCATGTGGCAAAAGGTGCCAAATAATACCTCACCAAACTGTGGCTGGCCCTGCTGGC	901200
Qy	6601	agcgcgcttgcgcaagccgagcttgcgcgcgacatgatattggccgcgcgcgcgcgaagcgcggt	6660
Dh	90121	AGCGCGCTTGGCCAGGCCAGCTGCCCGGCAATGATTGGCCCGCCCGAGAGCCGGGGGG	901800
Qy	6661	gtcgcgcggaacacctctctctctctcccatctccctcagagccaatgttgaagaagggaag	6720
Dh	90181	GTTCGAGCGGAAACCTCTCTCTTCCCTCCATGCGCTTGAGGCCATTTGGAGAAGCGAAAG	902400
Qy	6721	tgaagctgcgcgtgttctactctgcctctcaactttgattgaagagcggttaattaaagt	6780
Dh	90241	TGAAGCTGCGGCTGTCTACTGCTCCCTTACTTTGATTGAAGCAGGCCCTAGTAAAAAG	903000
Qy	6781	ggtttttgggacctcaagtgccttaagaatgatgcgcgacaaattctctgtctctttact	6840
Dh	90301	GGTTTTGGGCTTCAGTGCTTAAGATATGATGCCGACAAATCTGTCTCTTTTCACT	903600
Qy	6841	ggaagctcgttagcggaagacatacagaatttgatgtaactctctctatctgtctttat	6900
Dh	90361	GGAAGCTGCTGAGCGGAGAACTACAAATGATGATCTTCTCTACTCGCTTTTAT	904200
Qy	6901	cccttagcgacttaagatctgttlaagatggcccggaatgatctctcagggttgaaaggga	6960

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Oy	8041	gaagccttaaaagtggtgtagggattcaacggttcctccctcccacccttgaaaaacaact	8100
Db	91561	GACCCTTAAAGGTGGTAGGAGTTTCACGTTCTCTCCACCCTGGAAAACACTT	916220
Oy	8101	ggcatttacagtttcgtagtagactttcttaaacaacacctcagtacttggggagacag	8160
Db	91621	GGCATTTCAGTGTTGGTAGTAAGTTTCTATAAACAACCTTCAGTACTTGGGGGAACG	91680
Oy	8161	tattccaactttttcgtttttgcataaacatlttttttttggagatctcagtcagccga	8220
Db	91681	TATTCACACTTTTTTGGTTTGCATTAACATTTTTTTTTGAGGATCTAGCTCACGCCCA	91740
Oy	8221	gtcaacctaanaaaggtttggtttctcttaaaaaatgaagctacttagtaagfcttttgttt	8280
Db	91741	GTCNACTAAAAAGTTTGGTTTCTTTAAAAATGACGTACTTAAAGGCTTTTTTGTTT	91800
Oy	8281	cttccctgatcacctctcatltaactcttctctcttctactttggagaatacggcaacaacatcat	8340
Db	91801	CTTCCTGTATACCTCTTCACTTACTCTTCTCTTCTATTGGAGATAGCGCAACAACATCAT	91860
Oy	8341	aaaattttttctttcccaagttttgccacttgttaattaaagtgtttgtctctcat	8400
Db	91861	AAAAATTTTTTCTTCCAGTTTGGCACTTGTGCACCTGGTAGTAAAGAAGTGTGTCTCTCAT	91920
Oy	8401	tgtttttgattccaagtaaaagaaagaaatgaatatcctcatcacacaacacagttctgtt	8460
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Oy	8461	ttgtaaattattttaagaaaagttagcatgcaaatttttaattctcttttagtvtctoaagt	8520
Db	91981	TTGTAAATATTATTAAAGAAAGTTTACATGCAATTTTTTAACTCTTTTGTGTCTCCAGT	92040
Oy	8521	aaaataagcataacatttggttttaaaaaactaataaaaatgaagcaaaaacccctttta	8580
Db	92041	AAAAATACCAATRCATTTTGTATTATAAAACTAAATPAAAAATAGCAAANAATCCCTTTGA	92100
Oy	8581	tcocctcccatltaacttctactccgcacccctagaataataltttctgtttttctgaaba	8640
Db	92101	TCCCTCCCATTCATTAATTCACCTCCGCACCCCTTAGAAATATATTTTCTGTTCGAATA	92160
Oy	8641	ttcttcccgaccttttggtttggcatcttctacaagctacatatgtacaatgvcggy	8700
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Oy	8701	ggtgtgtgtgttggttgtgtgtgtatgaagagacacccbtgagtgcatgtgtcatattgra	8760
Db	92221	GGTGTGTGTGTGTGTGTGTGTATGAGAGAACACCTGTAGTCATGTGTGTATGTGA	92280
Oy	8761	aacatttgttctactctctccacatttggagatctttccatvgcgsgtaaaaaatagatlga	8820
Db	92281	AACATTGTTTTCACCTTCCACATTTTGGAGATCTTCCATGGCAGTAAAAATGATTTGA	92340
Oy	8821	tttgbtcttttaaatattatacagtagtaglaacattatgaagtaccataggttactcaac	8880
Db	92341	TTCTGTCTTTTAAATATTATTAACATAGTAGGTAACTATGAACTATACCATRAGGTACTCAAC	92400
Oy	8881	ctttctctcttaagtagagacgttcgcsccttaacagcatltaatgaaacatcatcttcaagc	8940
Db	92401	CTTTCTCTTTTAAGTAGAGCTTGGCCCTTACGCATTTTAATGAACATCATTTCTACAGC	92460
Oy	8941	ttctgtgcattgttgttagaataagtlacagtagtgggttatcaatcatltaaaatlga	9000
Db	92461	TTCTGTGCATTTGTTGTAGAGATACTACTAGTGGTGATTAATACATTTTAAATTTGA	92520
Oy	9001	catagcctgagtgctggtttttaaaactatttccccaaaaaagtgfgcagtaatttctttta	9060
Db	92521	CATACCTCGAGCTGTGGTTTAAAACTATTTTCCAAAAAANAGTGTGCAGTATTTCTTTTA	92580
Oy	9061	gaattattcttcgagaaagaacacttaatttagctcttaataaaaaaagcttbaacttgt	9120
Db	92581	GAATTATTTTGGGGGAAAGAACTTAATTTTAGCTTAATPAAAAACAACGTTAAACATGTGT	92640

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QY 10321 atatttaaaataagatgtctatctacaggggttgaagtttaagttatttctgatac 10380  
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RESULT 2  
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 AC012066 unorderd pieces.  
 AC012066 VERSION AC012066.2 GI:6139271  
 HTG: HTGS\_PHASE1.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 184421)  
AUTHORS Waterston,R.H.  
TITLE The sequence of Homo sapiens clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 184421)  
AUTHORS Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (19-OCT-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT  
On Oct 29, 1999 this sequence version replaced gi:6067197.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

FEATURES  
1 184421: contig of 184421 bp in length.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="NH0173H09"

BASE COUNT 52772 a 36593 c 38351 g 56475 t 270 others

ORIGIN

Query Match 7.6%; Score 1427.4; DB 42; Length 184421;  
Best Local Similarity 65.6%; Pred. No. 2.7e-225;  
Matches 2739; Conservative 0; Mismatches 1216; Indels 222; Gaps 36;

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Db 33751 CTGATTCTTTTCTTCTGATGAGTACCTCCATTGTGTAATGATACCAATTTTC 33810  
QY 14643 tttaacctgtcatcattctgtatgacacttagtgcattgattccatacatcttctgttgat 14702  
Db 39811 TTTATCCATTCATCTGTGATGACACTTAGGGTGTCCAAATTAATGATATGTTAAT 39870  
QY 14703 agtgcctgcagtaaacatactcgtgacacatactctttagataatttaattc-cttccctt 14761  
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[illegible]

REFERENCE	1 (bases 1 to 223542)
AUTHORS	Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,J., Chen,Z., Culpepper,P., Ding,Y., Dugan,S.P., Durbin,K.J., Forcum,J., Genseth,R.P., Garcia,C., Garcia,D.K., Gorrell,H., Gorrell,L.L., He,X., Hernandez,J., Jackson,L.E., Kondajewski,N., Leal,B., Licharge,O., Liu,W., Logan,O., Lu,J., Martinez,C., Moore,S., Moorish,T., Nguyen,N., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.M., Rashid,N.D., Rives,C.M., Scherer,S.E., Shen,H., Simon,M.L., Vo,Q.K., Wei,Y., Williamson,A.L., Worley,K., Zhou,X., Naylor,S.L. and Gibbs,R.A.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 223542)
AUTHORS	Morley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 223542)
AUTHORS	Morley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (01-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Apr 2, 1999 this sequence version replaced g14454420. INFORMATION: <a href="http://www.hgsc.bcm.tmc.edu/or_email/gc-help@bcm.tmc.edu">http://www.hgsc.bcm.tmc.edu/or_email/gc-help@bcm.tmc.edu</a>

**CLONE LENGTH:** This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

**ANNOTATION OF FEATURES:**  
 STRs are identified using ePCR (genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.  
 Repeats are identified using RepeatMasker (A. Smit and P. Green,

unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarly (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES		QUALSPAT-REPORT.
SOURCE	Location/Qualifiers	
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repeat_region	complement(872..1070)	/rpt_family="MLT1G"
repeat_region	1076..1373	/rpt_family="ALuDb" complement(1378..1441) /rpt_family="MLT1G"
repeat_region	/rpt_family="MLT1G"	complement(2134..2163) /rpt_family="("TA)n"
repeat_region	2512..2680	/rpt_family="("TA)n"
repeat_region	3310..3651	/rpt_family="MIR"
repeat_region	3877..3916	/rpt_family="AluSq"
repeat_region	4184..4451	/rpt_family="L2"
repeat_region	4454..4801	/rpt_family="LIME3"
repeat_region	4826..4942	/rpt_family="MER7A"
repeat_region	5055..5174	/rpt_family="LIME3"
repeat_region	5189..5485	/rpt_family="FLAM_C"
repeat_region	5486..5947	/rpt_family="AluDb"
repeat_region	5948..6589	/rpt_family="LIME3"
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repeat_region	7392..7481	/rpt_family="("TA)n"
repeat_region	7482..7795	complement(7495..7795) /rpt_family="AluY"
repeat_region	complement(7807..8100)	complement(7807..8100) /rpt_family="AluXs"
repeat_region	complement(8843..9142)	complement(8843..9142) /rpt_family="AluXs"
repeat_region	9835..10116	complement(10937..11242) /rpt_family="AluSq"
repeat_region	11547..11628	complement(10937..11242) /rpt_family="AluSq"

[illegible]



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 Qy 17069 tcaatgcttctgcccctcctcctcctcctcctcctcctcctcctcctcctcctc 17128  
 Db 179666 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 179725  
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 Qy 18190 gtttcaaaaatttgtaagcttcttcttggtcgtcgtcgtcgtcgtcgtc 18249  
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 Qy 18370 tcttctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 18426  
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 Db 181065 TCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 181122  
 Qy 18547 ttaattatataacagcctcctcctcctcctcctcctcctcctcctcctc 18591  
 Db 181123 TTTACCATTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 181167

RESULT 4  
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 DEFINITION Human DNA sequence from clone 154J13 on chromosome Xq26.1-26.3,  
 complete sequence.  
 ACCESSION AL049734  
 VERSION AL049734.11 GI:5791525  
 KEYWORDS HNC.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 126766)  
 AUTHORS Bird,C.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 COMMENT On Aug 27, 1999 this sequence version replaced gi:5777846.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 EMBL, SW, SWISSPROT, Tr, TREMBL, Wp, MORPEP, Information  
 on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence is

the entire insert of clone 154J13. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>

154J13 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:pcrYAC2>.

location/Qualifiers

## FEATURES

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/clone\_lib="RPCI-1"  
/clone="RPI-154J13"

BASE COUNT 41677 a 24251 c 24278 g 36560 t  
ORIGIN

## Query Match

6.7%; Score 1262.4; DB 11; Length 126766;  
Best Local Similarity 62.4%; Pred. No. 3.3e-198;

Matches 2613; Conservative 0; Mismatches 1361; Indels 214; Gaps 32;

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QY 14642 cttaactgttaacccatgtagacacctaagtgtagtccatcttctgtgtgaa 14701
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QY 14702 tagtgcgcgaataacatactgtagacatacttt-tagaataataattcttctt 14760
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QY 14761 ttgtgaaatctagtgtagtggaatgctagatggaagatagttctattttaa 14820
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Db 64026 TGAGAAATGTCGTTCTATTCCTTTGCCACTTTTATGATGGGTTGTTGTTTTTT--C 63969

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QY 15166 tttagcagatatcttctgcatcacaagatgtgtctctcctcaactgttattctt 15225
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QY 15272 ----- 15272

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QY 15380 tggatatctaatttctcagacacatgattgaagagglttctggttccacagtgatgt 15439
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QY 15680 gtttttcttaatttgcacaaaaatlaactgtgatttgaataagattgatatagaatg 15739
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Dd	60511	cacatatattgtttgttgctgctatctatctatctatcttttttaggtttgtaatttttttaa	60452
Oy	18477	ctcttaagtaactccagtgctgcgggtgcacaatgat----ttgaattgttatatctctt	18532
Dd	60451	attttggagacctccattgattgagctgcataatatttttagcatttgatttgatattttccct	60392
Oy	18533	gttgattgctgtctcttataatataaagcattcttaagccttt	18580
Dd	60391	gtttggacaaagcctttttatcactaatatattgctccctttttgtcttttt	60344
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DEFINITION	HS20J23	137111 bp	DNA PRI 23-NOV-1999
		Human DNA sequence from Clone 20223 on chromosome Xq26.2-27.2	
		(ras-like protein TC25) EST, CA repeat, STS, CpG island, complete	
ACCESSION	AL022576.1	GI:3286426	
VERSION	AL022576		
KEYWORDS	HTG; P21-RAC1; ras-like protein TC25; repeat polymorphism.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Primates; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Placentalia; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 137111)		
AUTHORS	Pearce,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-JUL-1998) E-mail enquiries: humquerry@sanger.ac.uk		
COMMENT	Clone requests: clonequery@sanger.ac.uk On Jul 4, 1998 this sequence version replaced gi:3250824. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 20223. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/ChrX">http://www.sanger.ac.uk/HGP/ChrX</a> 20223 is from the library RPCL1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <a href="http://bacpac.med.buffalo.edu/VECTOR.pcrPAC2">http://bacpac.med.buffalo.edu/VECTOR.pcrPAC2</a> .		
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	complement(1..149)		
repeat_region	/note="L1PA12 repeat; matches 769..613 of consensus"		
repeat_region	complement(442..743)		
repeat_region	/note="Alusx repeat; matches 302..1 of consensus"		
repeat_region	complement(746..1024)		
repeat_region	/note="L1MK1 repeat; matches 488..206 of consensus"		
repeat_region	999..13711		
repeat_region	/note="WSTD repeat; matches 1..394 of consensus"		

repeat__region	2309. .2392	/note="MERB repeat: matches 85. .170 of consensus"
repeat__region	complement(2464. .2568)	/note="MERB repeat: matches 109. .4 of consensus"
repeat__region	complement(3029. .3355)	/note="11ME2 repeat: matches 910. .581 of consensus"
repeat__region	3382. .3687	/note="AluY8 repeat: matches 1. .303 of consensus"
repeat__region	3688. .3713	/note="13 copies 2 mer ga 92% conserved"
repeat__region	4610. .4869	/note="MIR repeat: matches 3. .261 of consensus"
repeat__region	6094. .6242	/note="MIR repeat: matches 2. .151 of consensus"
repeat__region	6244. .6551	/note="AluY8 repeat: matches 1. .308 of consensus"
repeat__region	7075. .7340	/note="AluY8 repeat: matches 1. .269 of consensus"
repeat__region	7348. .7562	/note="MIR repeat: matches 33. .245 of consensus"
repeat__region	7563. .7898	/note="1HEB repeat: matches 28. .364 of consensus"
repeat__region	complement(7965. .8367)	/note="L1B repeat: matches 390. .1 of consensus"
repeat__region	complement(9128. .9394)	/note="AluY8 repeat: matches 292. .2 of consensus"
repeat__region	complement(9943. .10412)	/note="11ME2 repeat: matches 1047. .559 of consensus"
repeat__region	complement(10334. .11316)	/note="L1P2 repeat: matches 891. .1 of consensus"
repeat__region	complement(11167. .11451)	/note="11 repeat: matches 5390. .5107 of consensus"
repeat__region	11493. .11538	/note="73 copies 2 mer ta 89% conserved"
repeat__region	complement(11569. .12007)	/note="11ME2 repeat: matches 540. .99 of consensus"
repeat__region	complement(12010. .12308)	/note="AluY8 repeat: matches 302. .1 of consensus"
repeat__region	complement(12309. .12352)	/note="11ME2 repeat: matches 113. .70 of consensus"
repeat__region	complement(12353. .12436)	/note="AluY8 repeat: matches 291. .208 of consensus"
repeat__region	complement(12438. .13219)	/note="11 repeat: matches 5316. .4522 of consensus"
repeat__region	13425. .13456	/note="16 copies 2 mer tt 84% conserved"
repeat__region	complement(13460. .13735)	/note="AluY8 repeat: matches 301. .14 of consensus"
repeat__region	complement(14013. .14115)	/note="MIR repeat: matches 216. .122 of consensus"
repeat__region	14133. .14172	/note="70 copies 2 mer ac 98% conserved"
repeat__region	14304. .14366	/note="MIR repeat: matches 84. .146 of consensus"
repeat__region	complement(16096. .16450)	/note="11ME2 repeat: matches 676. .321 of consensus"
repeat__region	complement(16561. .17023)	/note="MIR repeat: matches 146. .84 of consensus"
repeat__region	18418. .18691	/note="AluY8 repeat: matches 1. .289 of consensus"
repeat__region	complement(22513. .22719)	/note="MIR repeat: matches 218. .4 of consensus"
repeat__region	complement(23373. .23570)	/note="AluY8 repeat: matches 300. .3 of consensus"
repeat__region	complement(24714. .24784)	/note="MIR repeat: matches 146. .76 of consensus"
repeat__region	25015. .25073	/note="MIR repeat: matches 40. .97 of consensus"
repeat__region	25807. .25941	/note="MIR repeat: matches 24. .146 of consensus"
repeat__region	25992. .26090	/note="MIR repeat: matches 91. .188 of consensus"
repeat__region	complement(26496. .26636)	



repeat_region	/note="MIR repeat: matches 206. .58 of consensus" 27159. .27176 /note="19 copies 2 mer gt 100% conserved"
repeat_region	28069. .28101 /note="MIR2 repeat: matches 114. .146 of consensus"
repeat_region	28699. .28895 /note="MIR repeat: matches 1. .202 of consensus"
repeat_region	28896. .29430 /note="MLR2D repeat: matches 1. .534 of consensus"
repeat_region	29439. .29487 /note="MLR2CA repeat: matches 455. .503 of consensus"
repeat_region	29489. .29557 /note="MLR2 Internal repeat: matches 2. .70 of consensus"
repeat_region	29556. .29827 /note="MLR2 Internal repeat: matches 272. .535 of consensus"
repeat_region	29825. .30065 /note="L1 repeat: matches 5150. .5389 of consensus"
repeat_region	29917. .30434 /note="L1PA2 repeat: matches 1. .517 of consensus"
repeat_region	30437. .30735 /note="Ally repeat: matches 1. .299 of consensus"
repeat_region	30736. .31114 /note="L1PA5 repeat: matches 510. .888 of consensus"
repeat_region	31125. .31200 /note="MLR2 Internal repeat: matches 537. .609 of consensus"
repeat_region	31217. .31283 /note="MLR2G repeat: matches 321. .388 of consensus"
repeat_region	31231. .31283 /note="MLR2CB repeat: matches 453. .501 of consensus"
repeat_region	31561. .32214 /note="MER42C repeat: matches 573. .1254 of consensus"
repeat_region	32196. .32310 /note="MER42C repeat: matches 1292. .1404 of consensus"
repeat_region	32309. .32350 /note="MER42C repeat: matches 1489. .1530 of consensus"
repeat_region	32612. .32654 /note="MIR repeat: matches 153. .110 of consensus"
repeat_region	32808. .32875 /note="L1PA7 repeat: matches 829. .892 of consensus"
repeat_region	33035. .33138 /note="MIR2 repeat: matches 43. .146 of consensus"
repeat_region	33421. .33615 /note="MIR repeat: matches 12. .206 of consensus"
repeat_region	33612. .34003 /note="AlusX repeat: matches 297. .1 of consensus"
repeat_region	34219. .34518 /note="AlusX repeat: matches 301. .1 of consensus"
repeat_region	35069. .35315 /note="MIR repeat: matches 1. .257 of consensus"
repeat_region	37050. .37655 /note="MLR1E repeat: matches 568. .1 of consensus"
repeat_region	37846. .38151 /note="AluDo repeat: matches 302. .1 of consensus"
repeat_region	38323. .38623 /note="AluDo repeat: matches 294. .1 of consensus"
repeat_region	39065. .39370 /note="AluDo repeat: matches 1. .299 of consensus"
repeat_region	39821. .40052 /note="AlusX repeat: matches 292. .38 of consensus"
repeat_region	40265. .40449 /note="AlusX repeat: matches 302. .122 of consensus"
repeat_region	40451. .40549 /note="AlusX repeat: matches 4. .102 of consensus"
repeat_region	40951. .41602 /note="L1MB5 repeat: matches 267. .921 of consensus"
repeat_region	41614. .41878 /note="AlusG repeat: matches 300. .38 of consensus"
repeat_region	42197. .42488 /note="AluDb repeat: matches 1. .291 of consensus"
repeat_region	43197. .43411 /note="MER20 repeat: matches 2. .218 of consensus"

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DB 59725	CATGACACATCATCTTTTAAAGCGCATAGATTCCAAAGGTGATATGTCACCATTTT	59784		
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DB 59785	CTTTATATGATGATGATGTTGATGGGCATTTGGGTGGCTCCAAAGCTTTGATTTGTA	59844		
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QY 14761	tttgtaaaaatcctagtaagtgaggatgtctagatggaagaatagttctatctttaa	14820		
DB 59905	TGGGATATATACCCCATATGAGATGGATGGCGGCAATGATTTCTGCTCATATCTT	59964		
QY 14821	gggaattcccatctactgttttcccaagaaggtctgtaactaatccaatcccaatgta	14880		
DB 59965	GAGGAATGCTACACTGCTCTCCACAAAGTGTAATTATATACACGCCAACCACTG	60024		
QY 14881	tataagagcttcccttttttccacatgataaccaca-----ttgtcgtctttaat	14933		
DB 60025	TAAAGCATTCCTATTCTCCACATCCTCCAGCATATATGTTTCTGACTTTTAT	60084		
QY 14933	aaaagacattcctgactagatagaaggctgatactcatctatgtgaattgattctctc	14993		
DB 60085	GATTCGCATTTCACTGATGCTGTAAGATGCTATCTCATTTGGTTGATTTGCATTTCTCT	60144		
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DB 60323	ATTGCAAAAATTTTCTCCATTTCTTTAGG--TTGCCATTCACCTTTACGATAGCATCTT	60381		
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DB 60382	TGCTGTGCAGAAAGCTTTAGTTGAATTAGATCCATTTGTACAGTTTGGCTTTGTGTC	60441		
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DB 60442	CATTGCTTTGGTTTATGATGATGAGCTTTTGCCCATGCCATGACTAGATGATATGC	60501		
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DB 60502	CTAGGTTTCTTCTAAGGCTTTTAAATGATGATGATGCTTTAATTAATGCTTTTATTCAT	60561		
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DB 60562	CTTAGATTATTTTGTATAG--GTGTAAGAAAGGGGTCCAGTTTCAAGTTTCTGACAT	60620		
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DB 60621	GGCTAGCCAGTTTCCCAACACCATTTATGAAATAGGCGACCTTTCCCATCTGTTT	60680		
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Db	62834	CTTTATATAGTCGGGTAGGGGTATCATATTTGTGTA--TCTTCAAAAATCAGTCCCT	62891
Qy	17765	catctcatgaaccttctgtg99gttttttttttcacgacatctcatcttagctctctc	17824
Db	62892	GGATTCATTGATTTTGTGAAGGTTTTCAT---CTCTTATATCCTTCAGTCTGCTCTC	62948
Qy	17825	gactc---tcatcttctctctctcgtcagcttllgggttttctgttttcttgctcgt	17881
Db	62949	GATCTTAATTATTTCTTGCTCTCTCTACTACTGTAATTTGTTTCTCTTGCTTCTCTA	63008
Qy	17882	ttcccgagggtgcgtctctagatcttaactgttaactcttctcccttttgatga9a	17940
Db	63009	TTCTTTTATTTTGTATGTTGGAGTGTCCACTTTAGATCTTTCTCTGCTTCTCTTGGG	63068
Qy	17941	attatctgc---gtgtctctcttagacagctctttgctgatacccaaggttttgata	17996
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Qy	17997	tggtggtttacatttctatttggtttcaaaaacatttttttaattcttgccttaattc	18056
Db	63129	CATTATATCTTTGTTCTCATTTGGTTTCAAGAACTTATTT--ATTTCGCTTAAATTTT	63185
Qy	18057	ttcatctgacctatctgtcatccaagagcagtgtgtttaaictgttgataattgtaaggt	18116
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Qy	18237	ctgtctcttgagaagtcttcacatacgtctgataagaatacttatactcgcagtgttgat	18296
Db	63365	CAATTTTGAATTAATGCAATGCAATGAGGTGCTGAGAAGATATATATCTGTGGATTTGGGTT	63424
Qy	18297	agaatgttttgtaaatgctcgtgttaagttcaatttggtctaaagtccagtttaagtcaggtg	18356
Db	63425	GGAGAGTTCGTGAGATGTCATTTAGGTCCACTGTGGCCGAGACTGAGTCAATCCCTGGA	63484
Qy	18357	tttcttgctgattctctgtctcagatagtactgtcctaagctcgtlaagtggtgttaatt	18416
Db	63485	TATCTCTTTAATTTTTCGCCCTGTGTGATCTGTCTAATATTGACAGTGGGATGTTAAAT	63544
Qy	18417	ttcacac--fatgtgtctcagtgatctctcttcttagctcagtaactgtttta	18473
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Qy	18474	tgaactcttagtaactccaatgctgggtgcaaatatgattttaaatgttatatatattcttg	18533
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ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE	1 (bases 1 to 81746)
JOURNAL	DOE Joint Genome Institute.
REFERENCE	Sequencing of Human Chromosome 5
AUTHORS	Unpublished
TITLE	2 (bases 1 to 81746)
JOURNAL	DOE Joint Genome Institute.
COMMENT	Direct Submission Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA <a href="http://www.jgi.doe.gov">www.jgi.doe.gov</a> . * NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * * 1 744: contig of 744 bp in length * gap of unknown length * 745 791: contig of 47 bp in length * gap of unknown length * 792 2306: contig of 1515 bp in length * gap of unknown length * 2307 4822: contig of 2516 bp in length * gap of unknown length * 4823 7872: contig of 3050 bp in length * gap of unknown length * 7873 11199: contig of 3327 bp in length * gap of unknown length * 11200 14451: contig of 3252 bp in length * gap of unknown length * 14452 23678: contig of 9227 bp in length * gap of unknown length * 23679 42525: contig of 18847 bp in length * gap of unknown length * 42526 81746: contig of 39221 bp in length. * Location/Qualifiers * 1..81746 * /organism="Homo sapiens" * /db_xref="taxon:9606" * /clone="CIT97SKB_65D22" * /ORIGIN
BASE COUNT	26272 a 16958 c 16418 g 22092 t 6 others
Query Match	6.6% Score 1242.4; DB 41; Length 81746; Best Local Similarity 65.2%; Prid.No. 6.3e-195; Matches 2701; Conservative 0; Mismatches 906; Indels 535; Gaps 38
OY 14584	tgaattcattcttggttgcgcatgatccatctgatatataaccacatttc 14643
Db 20039	TTATTTCACAGTATTTTATGCGTAGTGATTTCCATGGTGATATCACATTTCT 19980
OY 14644	ttacctgtcacacatgatgagcaacttagtgttccatactcttgctgtgaata 14703
Db 19979	TTATCCACTCATGTGATTGATGAGCACTTGAGACCGGTTCCATTTTTTGGCGGTGAAT 19920
OY 14704	gtgcgcgtaaacactatgagcacatacttttagtatattaattcttctttt 14763
Db 19919	GIGCTGCTAATAACGTGCAGCGCAAGTGTCTTTTCATGTAAAGACTCTTTTCCCTTTCA 19860
OY 14764	gtaaaactagtagtgaggatcgccagatgaaagaatagtctacatttaattctgag 14823
Db 19859	GTAGATACCAGTAGTAGATTAATGATCAACAACGGTAGATCTACTTAACTTTAAAG 19800
OY 14824	aacttcacatctgtttccataagggctgtgctaattatctcccacaatgfatat 14883
Db 19799	GAATCCATACTGTTTCCATAGTGG-TGTAAGAATGTTTACATTTCCACCAACAGGTAA 19741



Db 17957 ATATGTTGGCTGTGTGTTTGTGATGGCTTTTA----CTTAAGGCATGTTCTTCT 17902  
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 Db 17901 ATGCTGATTTGCGAGGCTTGTCTCAT- AAAGGATGCTGGATTTTGTCAAAATGCTAT 17843  
 Qy 17050 ttcgcgtctaatagaagatcatatgttttgccectcattcgttgtatagatgctc 17109  
 Db 17842 TCTGTCTATATGAGATGATCCTGTGATTTTGTATTAATTCGTATATGCGAT 17783  
 Qy 17110 acatttttctgttcgaatgtgacatctcctcctcctcctcctcctcctcctcctcctc 17169  
 Db 17782 ACATTATATGCTGGGTATTTCAACACATCCCTGCAATCCCTGATTAACCCACTTGA 17723  
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 Db 17722 TCATGAGGTATATCTTATATATATGCTGTGATCCAGTTAAGTATTTCCGTTAAG 17663  
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 Qy 17290 tctctctcttctgt 17349  
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 Qy 17469 taataatctacgttaattcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 17528  
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 Qy 17821 cctcgtatct---tatcttcttctcctcgtctgtgtgtgtgtgtgtgtgtgtgtgt 17877  
 Db 17075 CTCGATCTTTGTATATTTCTTTCTCTGCTAGTGTGGTTGGTTGTCTGTCTTCT 17016  
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 Qy 17938 ggaatttatctgtg----tcttcttctgaaccttcttcttcttcttcttcttcttct 17993  
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 Qy 17994 gtaagttgttcttcaattcttcttcttcttcttcttcttcttcttcttcttct 18053  
 Db 16895 ATAGGTGTGTCT-CACATATATCATGCAATGATGAGAGGTTTAAATTTCCATCTCAT 16837

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 Db 16836 TTCAATGTTGACCCAGATCATTCAGAGAGATTTATTAATTTCCATGCAATTTTGCAT 16777  
 Qy 18113 gtttgtaattcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 18172  
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 Qy 18173 cacttgatgtatctcagtttcttcttcttcttcttcttcttcttcttcttcttcttct 18332  
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 Db 16300 TT 16299  
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 Euthalia; Primates; Catarrhini; Homindae; Homo.  
 REFERENCE 1 (bases 1 to 92171)  
 AUTHORS Sulston J.E. and Waterston R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 99063792  
 REFERENCE 2 (bases 1 to 92171)  
 AUTHORS Edwards J.  
 TITLE The sequence of Homo sapiens PAC clone DJ0903602  
 JOURNAL Unpublished (1999)  
 REFERENCE 3 (bases 1 to 92171)  
 AUTHORS Waterston R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 4 (bases 1 to 92171)  
 REFERENCE 4  
 AUTHORS Waterston R.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-1999) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

## COMMENT

On Feb 24, 1999 this sequence version replaced gi:3213073.

SUBMITTED BY: WUGSC  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

## VECTOR: pCYPAC2

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is DJ0901A04, 200 bp overlap.  
Actual start of this clone is at base position 1 of DJ0903G02;  
actual end is at 92171 of DJ0903G02.

## FEATURES

The location of this clone is unknown.

## source

1. 92171  
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/chromosome="unknown"  
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repeat\_region  
488..796  
/rpt\_family="Alu"  
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806..967  
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1029..1151  
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repeat\_region  
1167..1625  
/rpt\_family="Retroviral"  
misc\_feature  
1848..2014  
/note="match to EST AA078502 (NID:g1837976)"  
repeat\_region  
2015..2061  
/rpt\_family="(TGG)n"  
misc\_feature  
2048..2173  
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repeat\_region  
2230..2308  
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misc\_feature  
2745..3065  
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misc\_feature  
3352..3739  
/note="similar to EST AA487120 (NID:g2217284) ab19a07.s1"  
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8818..9026  
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10541..10643  
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repeat\_region  
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/rpt\_family="L1"  
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12245..12862  
/note="similar to EST T91861 (NID:g723774) yd54b06.s1"  
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12803..13004  
/note="match to EST T84729 (NID:g713081) yd54b06.r1"  
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12866..13336  
/note="match to EST AA373019 (NID:g2025561)"  
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12892..13309  
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QY	16138	ttcacacatgctggccaagatggtctcgcactctctgaccccttgatccacacaccccttgacc	16197
Db	20046	CATPAAGATGCTTTTCCATTGGTTGTGCTGCTCAATTTATTTTAACTGTTTGTGTGT	20105
QY	16198	tcccaaatgctcgggaattacaagcgtgagccacacacacccggccctttt-----tttt	16251
Db	20106	TTTCATGTGAGAGGTTTTTTTTTTTTTCCCAACCTTGSTTAAGTTATTTCCAGGTATT	20165
QY	16252	tgtaattgtaagctatgttaaatggagatggtcttgatcttggtgttcaatttgaaaca	16311
Db	20166	TTATTTTGTACCTATTGTAATAGAAATTCCTGCTTCTTTTATGATAG--TTTG	20224
QY	16312	ttatgtggtgtagaagaacacctaaatttgtagtgaatttgatatttgatcttgcaattta	16371
Db	20225	TTACTGGATATAGAAACATCACTGATTTTGTATGTGACTTTGTGCTTGAGAGCTTTA	20284
QY	16372	ctgaatt-----catttaaccaatctaagggttttttttttttttttttttttgaagaattt	16428
Db	20285	CGAATTAATACATCTGTTTTTTTAAATTTTTTTTATTTTATTTTGAAGACAGTCT	20344
QY	16429	caattgtgtgcccaagcgtgagttgcaatggaacaaatcgaagtcgaagctgtgct	16488
Db	20345	CCCTGTGTTGCCAGGCTGGAGTGCAGTATGCAAATCTGGCTCACTGCACCTCCGCT	20404
QY	16489	ccgggttcaaatgattctccggccctcagcccccggagtagctgggatttaagaagcatg	16548
Db	20405	CTGGGTTTCAACGATTCCTCTGCTTCAAGCTTCCCAAGTAGCTGGGATTACAGCACTTA	20464
QY	16549	ccacacacccggcctaattttgtagtttagtagaagaagggtttacacatgttgcca	16608
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QY	16609	-gtgtgtcttgaaactactgaactcgaagtgtatctgagccacactcgaagctcccaagtgtcg	16667
Db	20521	GGCTGTCTCAACACCTCCCAACCTCAGGTATCCGCCACTTGGCTCCCAAGTCTCG	20580
QY	16668	gattcaaggcatgagctacccggccgtgcaaatct-----aagaatttttggtg	16717
Db	20581	GATTAACAGGCAAGAGCTACCAATGCCAGCCTTAACCTATTAAAGGTTTTTGGGTG	20640
QY	16718	gagctcttaaggtttctct-----agataaagaatcatacatcaagaaacaggagaaat	16771
Db	20641	GAGTCTTTAGTTTTTCTGTTTACAAGTAAAGATATGATATGTCATCTGCCAAGAGACAAAT	20700
QY	16772	ttgaactccttcttataaattttgatgctcttgtttcaattctctgtgcgtgattgtctg	16831
Db	20701	TTGACTCCCTCTGTGCTATGTTGGAGTCCCTTATTTCTTATCTGTGATCACTCTG	20760
QY	16832	gttagaacctcaataactatctg---aagagtgtgaaagagagacactgttttctt	16888
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Db	20881	TAGCATATATGCTTTTCTATGTGTGAG--TGTCTCTTATGCTTAATTTGTGACA	20938
QY	17008	gttttctctataaaggagatgtgaatttataaattctttttgtgcgtctattaagatg	17067
Db	20939	GTTTATCATCATAGAGAAAGGTAAAGTTTATGAGATGATTTTCTGCATCTGTGAGTG	20998
QY	17068	atcataatggttttgccctcaactcgtgtgataatgatacaatttata--tttga	17126
Db	20999	ATCCAGATATTTTGTGCTCTCAATCTGTGTGATGTGATATACATGCAATGATTTTGTG	21058
QY	17127	taattgtaacctactctgataccctgataaacaacacactgataagtgataactt	17186
Db	21059	TATGTTGAGCACTTTTGATCTCTGAGATTAATCCCACTTGATATGATATTTATCTT	21118
QY	17187	ttgattttggttgagatttggtctgctgataattgttgaggattttgcatttggtt	17246

Db	21119	TTTCATTTCACTTAATGATTTGGCTTGGTAGTATTTATGCTGAGAAATTTTCCATCTGTATT	21178
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Db	21179	CATTA-----GGAATATGCGCTGATAGTTTCTCTTCTTGTTGTGTCCTGCTGATG	21233
QY	17307	gttataaggcgataatgaccttaagaataagtagaggagagccgtgc---ttgatt	17363
Db	21234	GATATCAGGATATCTGTGCTTAAACAATGATGAGAAAGATTCCTCCCTTCAAT	21293
QY	17364	ttttgaaatgattcagaagatattataactctctcttgtaacttgtagaatctg	17423
Db	21294	TTTGGGAATAGTTTGAAGAAGATTGCTGTTTCTTTCTTAACTGGTAGAAATCA	21353
QY	17424	gctgtgaagccatcgtgaactggtcttcttggttgaggagatgtaaaaattactgatt	17483
Db	21354	GCATTAAGC---CTAGTCTAGGCTTCTCTTGGGAGACATTT--TTGTACTGATT	21408
QY	17484	aattctgtgtctaatatgtgtcattcaagatttctgtctctctctgttcatcttg	17543
Db	21409	CAACCTGCTATCAATTTTGGGTGAGTTGAGTTTCTGTTCTTCCATAGTTCAATCTTG	21468
QY	17544	gtaggtgtgttttctgtggaatgtatcatctctgtgaagtttctgaattagtaat	17603
Db	21469	GTAGCTGTGATGTCTGGAGATTATCCCTTCCCTAAGTTTCCATTTGTTAGAT	21508
QY	17604	atagtcaattatagctgtgtagat---ctttgaactcgtgtgaatcagttgtaagt	17659
Db	21529	ATGGTGTGTAATAAGCCTTTAAACATCCCTTTATTTCTTGGTATACAGTTGTATAGT	21588
QY	17660	ctccttttcaattctgatttatttg-----ctcttcaccttcttct	17706
Db	21589	CTCCTTTTCAATTTGATGTATTTATTTGGGCTCCTCTTCTTCTTCTTCTTCTT	21648
QY	17707	tggttagctgaaagtgtgtatcaatttttttatacctcttgaggaaacacagctttca	17766
Db	21649	TGTATTAGCTCACTAGTGTGTTATCAATTTGTATTCTTTCAAAATAAACACTTTTA	21708
QY	17767	tttcaatgaactttgtgggttttttttttcaagccaatatcaattagttctgcctga	17826
Db	21709	TCTGTGTGATCTTTGCAATTTCTTTTGTGTC-----TCTGTGTGCAATTTGTGTTGCT	21759
QY	17827	tcttattcttcttctctgcagatttggtgttggttttcttggtttcttggttct	17886
Db	21760	TGTTTTTTTTTCTTTCTTAAATGTGTGTGTGTGTGTTCTTGTGCTTTTGAATCTCT	21819
QY	17887	cgaggtgcgtctttagattataactgtgaactctctc--ccttttgatgtagaattta	17945
Db	21820	TGAGGTATATCATATGAGTTGTTATTGAGATCTTTACAGTTTGTGGTAGGCATTTA	21879
QY	17946	ttgcgtgt-----gttctcttgaactgctttgtcgtgataccacagagtttgtagtg	18001
Db	21880	TGTGATTAACCTTCCTCCTACTACTGCTTGTGTGATACCATAGGTTTT--GC	



Db	22169	CTGGAGAAATGTTCCATGCTGGTTCATGATGAGATGAGATGTTGTTTCTGCTGCTGCTGATGAAAT	22228
Qy	18302	gttttgtaaatgctcgtttaagttcaattcgtctcctaagtcagglttaagtcaggctgttcct	18361
Db	22229	ATTCTGAAAAATATCTGTTAGGCTCATTTGGTCTTAAGTGCACCTTTAAATCTAATGTTTCT	22288
Qy	18362	ttgtctgattccttgcctcagaagatcctgtcctaagctgcctgaagtcggggtgttgaaatttcac	18421
Db	22289	TGTGTGATTTTATGCTCTGATGAAACTGTCACATGCTGACAGTGAAGGAAATGTGAAGTTCACA	22348
Qy	18422	act---atgtgtgcagatgatactccctcttctttaagtcagtcagaactgttttagact	18478
Db	22349	ACTATCATTGTATTTGATGCACTCTATCTCTCCCTGTACATTTAAATAATTTGGCTATGCTGT	22408
Qy	18479	cttaagtaactccagctgtctgggtgtgcacaatatgtatttaagaattgttatatactctgtcgaa	18538
Db	22409	CTGGATGCACCTGTCTGTGGTTGCATGCA--TATTTAGAAATGCTTATATTTGTGCTGAA	22466
Qy	18539	tttgctcctttaatatataataagcaactctctaagctcttcttttttttttaactcgtt	18598
Db	22467	TTTATCCCTTTATATGATATATATATACCTCTCTTGTCTCTTTTACAGATTTTGA---CT	22522
Qy	18599	tttagatgctttcttcctcttgccatttttagagatcacactctcactttgaacttcagacag	18658
Db	22533	TAAAGTCGTTTATATCATGATGCAAGATTAGCTACCTGATTAACCTTTTGATTTCTGTTTG	22582
Qy	18659	tcctg 18662	
Db	22583	CGTG 22586	

REFERENCE	ORANISM	DEFINITION	LOCUS	COMMENT
HS13062	Human	DNA sequence from PAC 13062 on chromosome 6p22.2-22.3.	HS13062	
AL008627	Human	Contains ribosomal protein L29 pseudogene, ESTs and STS.	AL008627	
AL008627.1	Human	605 ribosomal; 6p22.2-22.3; L29.	AL008627.1	
GI:2769539	Human		GI:2769539	
605 ribosomal; 6p22.2-22.3; L29.				
Human sapiens				
Euchariota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
1 (bases 1 to 152077)				
Phillips, S.				
Direct Submission				
Submitted (02-JAN-1998) Chromosome 6 Project Group				
(http://www.sanger.ac.uk/HGP/Chr6/) Sanger Centre, Hinxton,				
Cambridgehire, CB10 1SA, UK. E-mail enquiries:				
humbug@sanger.ac.uk Clone request: clonequest@sanger.ac.uk				
On Jan 13, 1998 this sequence version replaced gi:12578053.				
IMPORTANT: This sequence is the entire insert of clone 130G2.				
During sequence assembly data is compared from overlapping clones.				
Where differences are found these are annotated as variations				
together with a note of the overlapping clone name. Note that the				
variations annotated may not be found in the sequence submission				
corresponding to the overlapping clone as we submit sequences with				
only a small overlap as described above.				
This sequence was generated from part of bacterial clone contigs of				
human chromosome 6, constructed by the Sanger Centre chromosome 6				
mapping group. Further information can be found at				
http://www.sanger.ac.uk/HGP/Chr6/				
This sequence has been finished according to sequence map criteria				
as follows. An attempt is made to resolve all sequencing problems,				
such as compressions and repeats, but not necessarily within known				
annotated human repeat sequence elements (e.g. Alu). Where the				
sequence is ambiguous, there is an annotation using the 'unsure'				
feature key.				
The true left end of clone 130G2 is at 1' in this sequence. The true				
right end of clone 130G2 is at 152077.				
130G2 is from the library RPCI1 constructed at the Roswell Park				
Cancer Institute by the group of Pieter de Jong.				
For further details see http://bacpac.med.buffalo.edu/.				

```

FEATURES
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/clone_1bp="RPC1-1"
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425..458
/note="17 copies of 2 mer 97 & conserved"
4098..4398
/note="AluXg repeat: matches 302. .2 of consensus"
5392..5501
/note="MIR repeat: matches 192. .81 of consensus"
5547..5848
/note="AluXg repeat: matches 302. .1 of consensus"
8419..8536
/note="MIR2 repeat: matches 146. .23 of consensus"
8556..8643
/note="44 copies of 2 mer 91 & conserved"
9351..9486
/note="MIR repeat: matches 117. .256 of consensus"
9897..9923
/note="9 copies of 3 mer 93 & conserved"
9934..10234
/note="AluJo repeat: matches 1. .298 of consensus"
10241..10541
/note="AluSg repeat: matches 1. .300 of consensus"
11340..11729
/note="MIR repeat: matches 82. .262 of consensus"
12202..12326
/note="MER3 repeat: matches 77. .199 of consensus"
12974..130234
/note="match: genomic DNAs B34759 279159"
13227..13338
/note="MIR repeat: matches 166. .48 of consensus"
13728..14019
/note="AluSg repeat: matches 1. .291 of consensus"
14020..14205
/note="MER3 repeat: matches 16. .199 of consensus"
1451..14966
/note="AluJo repeat: matches 300. .1 of consensus"
14997..15096
/note="MIR2 repeat: matches 25. .138 of consensus"
16165..16714
/note="MER7B repeat: matches 1. .558 of consensus"
16723..17020
/note="AluSp repeat: matches 1. .303 of consensus"
17047..17677
/note="MER7B repeat: matches 558. .1203 of consensus"
18315..18615
/note="AluYas repeat: matches 301. .1 of consensus"
18402..19737
/note="match: ESTs AA133590 W16581 AA133721 AA078850
R61223 AA513216"
20113..20755
/note="match: ESTs AA255497 AA256704"
complement(20536..21058)
/note="match: genomic DNA Z78827"
21004..21078
/note="MER5B repeat: matches 172. .96 of consensus"
complement(21079..21274)
/partial
/note="match: genomic DNA Z84499"
22029..22142
/note="MIR repeat: matches 148. .26 of consensus"
23045..23168
/note="MER5B repeat: matches 123. .1 of consensus"
23182..23267
/note="MIR repeat: matches 140. .65 of consensus"
24604..25009

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repeat_region	/note="ML1B repeat: matches 378. .167 of consensus" 25010. .23311
repeat_region	/note="A15x repeat: matches 302. .1 of consensus" 25312. .25478
repeat_region	/note="ML1B repeat: matches 176. .4 of consensus" 25785. .36076
repeat_region	/note="A15S repeat: matches 1. .292 of consensus" 28370. .28661
repeat_region	/note="A15S repeat: matches 300. .10 of consensus" 29395. .29675
repeat_region	/note="A15x repeat: matches 280. .1 of consensus; incomplete repeat" 30124. .30294
repeat_region	/note="M1R repeat: matches 212. .47 of consensus" 30359. .30654
repeat_region	/note="A15S repeat: matches 1. .302 of consensus" 31702. .33002
repeat_region	/note="A14Y repeat: matches 1. .301 of consensus" 33439. .33696
repeat_region	/note="L1ME3A repeat: matches 626. .887 of consensus" 33866. .33926
repeat_region	/note="MAE1 repeat: matches 13. .80 of consensus" 35804. .36654
misc_feature	/note="MER42C repeat: matches 710. .1333 of consensus" complement(36715. .37016)
repeat_region	/note="match: STS G13343" 38174. .38534
repeat_region	/note="L1B1 repeat: matches 902. .530 of consensus" 38536. .38579
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repeat_region	/note="L1B3 repeat: matches 538. .99 of consensus" 39206. .40096
repeat_region	/note="L1PA2 repeat: matches 891. .1 of consensus" 39947. .40655
repeat_region	/note="L1 repeat: matches 5390. .4684 of consensus" 40656. .44689
repeat_region	/note="L1 repeat: matches 5350. .1302 of consensus" 44356. .45318
repeat_region	/note="MER25 repeat: matches 2136. .1177 of consensus" 45304. .45764
repeat_region	/note="MER25 repeat: matches 1035. .561 of consensus" 45845. .46037
repeat_region	/note="MER25 repeat: matches 210. .13 of consensus" 46086. .46131
repeat_region	/note="M1R2 repeat: matches 94. .140 of consensus" 46306. .46424
repeat_region	/note="M1R repeat: matches 185. .67 of consensus" 46701. .46895
repeat_region	/note="M1R repeat: matches 46. .251 of consensus" 47169. .47461
repeat_region	/note="A14UB repeat: matches 1. .302 of consensus" 47457. .47674
repeat_region	/note="ML1D repeat: matches 4. .169 of consensus" 47697. .47948
repeat_region	/note="ML1D repeat: matches 243. .504 of consensus" 48306. .48403
repeat_region	/note="MER44A repeat: matches 1. .98 of consensus" 48408. .48666
repeat_region	/note="MER44B repeat: matches 284. .532 of consensus" 49741. .50223
repeat_region	/note="MLR2C repeat: matches 501. .1 of consensus" 52697. .52762
repeat_region	/note="M1R2 repeat: matches 137. .73 of consensus" 52851. .53032
repeat_region	/note="L1A4B repeat: matches 902. .1045 of consensus" 53192. .53238
repeat_region	/note="L1M2 repeat: matches 710. .666 of consensus" 53204. .53238
repeat_region	/note="L1M1 repeat: matches 700. .666 of consensus" 53242. .53646
repeat_region	/note="M1B repeat: matches 1. .426 of consensus" 53649. .54233

	Query Match	Best Local Similarity	Matches 2610;	Conservative	6.5%;	Score 1226;	DB 10;	Length 152077;	
repeat_region	/note="LMD2 repeat: matches 662, .53 of consensus"	55074, .55180							
repeat_region	/note="MIR repeat: matches 147, .20 of consensus"	57298, .57532							
repeat_region	/note="LORI repeat: matches 259, .1 of consensus"	58390, .58684							
repeat_region	/note="Aluio repeat: matches 1, .294 of consensus"	58925, .59124							
repeat_region	/note="MLTIF repeat: matches 541, .307 of consensus"	59122, .59381							
repeat_region	/note="MLTIF repeat: matches 277, .2 of consensus"	59382, .59437							
repeat_region	/note="28 copies of 2 mer 91 % conserved"	60759, .60928							
Query Match	6.5%;	Score 1226;	DB 10;	Length 152077;					
Best Local Similarity	61.7%;	Pred. No. 3,1e-192;							
Matches 2610;	Conservative	0;	Mismatches 1410;	Indels 208;	Gaps 33;				
QY 14582	cctgattcatctcttggtatgctgtaagtagtatccattggtatataataccacattt	14641							
DB 39518	CATGAACATCATTTTTTATGCTGCTACTACTATCCAGGCGTATATGCGCCACATTTT	39577							
QY 14642	cttccctggttccattccattgtagagacacttaggtttgattccatacttgcctgttgtaa	14701							
DB 39578	CTTAATCCAGTGTATCATGTTGTTGAGCATTTGGTGGTTCCAAGCTTTGCTATTGTGTA	39637							
QY 14702	tagtctcagtaaacatctatgctgtaacatacttt-tagaataattaattcttctt	14760							
DB 39638	TAGTCTTGCAATTAACATACATACGCTGCTAGTCTTTATAGCAGCATTTTAACTCCT	39637							
QY 14761	tttgtaaaaatctagtagtggaattgctagatgtaagaaatagttctatactttaa	14820							
DB 39698	TGGGTATATACCAATTAATGAGATGGATGGCGGCAATGATGTATTCTAGTTAGATCCCT	39757							
QY 14821	gagaaatctccatctgltttccatagaggctgtactaatttaacttccaccaatgta	14880							
DB 39758	GAGGAATGCGCCACATGACTTCCACAAGGTGTAACATGTTACGATGCCACCAACAGTG	39817							
QY 14881	tataagagttcccttttttccatagataaccaaa-----tgctgtctttaa	14933							
DB 39818	TAAAGGTCTCTATTTTCCACATCTCTCCAGACACTCTGTTTCCGATTTTAA	39877							
QY 14934	aaaagacattcgcataagataagtgatcatctcattgtaattgattgattcctct	14993							
DB 39878	CATTGCCATCTCAACTGCGTGAATGGATGATCTAATTGGGTTTGATTGCAATTCCT	39937							
QY 14994	tatgactgtaattgttgagcatttttccatataccctgttg-----gtatgctt	15045							
DB 39938	GATGCCAGTATGCTGAGCATTTTTCATGCTGTTTGGCTGCATAAATGCTCTCTTT	39997							
QY 15046	tgaaaaagtctatcatcagtgttttgctactttttaaagattgttagatttttgg	15105							
DB 39998	TGAGGAAGTCTGTTTCATGCTTCTTGCCACACTTTTGAATGGGCTGTGTTTTT-C	40055							
QY 15106	ttgttgatcgtttgagttccctgtgtatgctggaattatagccctgttgatgaataa	15165							
DB 40056	TTGTAAATTTGTTTGTAGTTCAATTGATAGATTCGATATTAAGCCCTTGTGCAATAGTAG	40115							
QY 15166	tttgagatatttctgtccattcaacaggaattgtgtctcttcaactcgttattctt	15225							
DB 40116	GTTTGGAATAATTTTCTCCCATTTTGTAGG-TTGCTGTTCACTCGATGAGTGATGTTCTT	40174							
QY 15226	tgcctgcaagaagctttttagttatttagtgagccatttgttgt-----	15272							
DB 40175	TGCTGTGCAAGAGCTCTTATTAGTTAACTAGATCCCAATTTGTCAATTTTGGCTTTGTTGC	40234							
QY 15272	-----ctctagatcttataagttttgggtcttacaacttaagcttcaatca	15319							
DB 40234	CATTGCTTTTGGTATTTTAGACATGAAGCTTGCCATGCTATGCTCTGAATGGTAA	40294							
QY 15272	-----	15272							

Db 40295 GCCTAGGTTTCTCTAGAGGTTTATGTTTATAGCTCAAGCTGAAGCTTTATCA 40354  
OY 15320 ccttgagtgatgttttaagtattagtgagagataagattcaattcattcttcgata 15379  
Db 40355 TCTTGAATGATTTTGTATAT-AGGTGTAGGAAGGATTCAGTTTCAGCTTTACATA 40413  
OY 15380 tggatataatattcttcagaccatttgagaagggttccgttccacagtgatgt 15439  
Db 40414 TGGCTAGCCAGTTTCCAGCACCATTTATTAATAGGGAATCTTCCCTCCCTCTGT 40473  
OY 15440 tcttgccgcttgccaacacagcttgccgaagtatgcggcttattcttcggcttct 15499  
Db 40474 TTTTCTCAGGTTTGCAGAGATCAGATGTGTAGATATGTGCTATTATTCTGAGGCT 40533  
OY 15500 ctatgcttgatccattgaccctgctgcttatttataccagtaacctgctgctt 15559  
Db 40534 CTGTCTGTTCCATGATTTATATCTC-TGTTTGTGTACAGTACCATGCTTTTGGT 40592  
OY 15560 agtataagcttgataataattgaagttagataatgtagccctgattattctt 15619  
Db 40593 ACTGTAGCTTGATAGTATAGTTTGAAGTCAAGTCAATGATGCTCCAGCTTTGCTTT 40652  
OY 15620 tctgctcagcattgcttgccatttgagggtctcttcttgctccatagtaatttagat 15679  
Db 40653 TGGAT--ATCTCTTGTGAGATAGTCAATTCATCTTGGCTCATCTTTTCATGGAAT 40710  
OY 15680 gtttttctaatcttgcaaaaaataacttggtatttgataggaat----- 15727  
Db 40711 GTTGTGTTGTTTGTGCCATTTGAGTTCTTTGTAGATCTGTGATTTAGTCCCTTGT 40770  
OY 15727 ----tgataagataatgagccttgctgtaagtagtcatttaattgattctct 15782  
Db 40771 CAGATATATATATGTGAAGATTTTCCCATCTGTGGTGTGTGTTAACTCTTATTT 40830  
OY 15783 gaataacagtagatcagtgagatgttttccatttgtagtca-aaattcttagc 15840  
Db 40831 CTTTGTGCTGTCAGAGCTTTTGTATTAGTAAAGCCCATCTATTATCTTTGTTTTC 40890  
OY 15841 tgttcttgtagtctcctctgtaggaatttaacctgctgtaataatactctgattgt 15900  
Db 40891 TTGCATTTGCTTTGGGTTCTTGTGTCATGAAGTCTTGTCCATAGCCAGTGTCTAAGGGG 40950  
OY 15901 gctgctgtagtctgctgcttcaattcttcttcttcttcttcttcttcttcttctt 15960  
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OY 15961 tctact-----ctgtcaccagccttgagtgagtgagtgagcaatcctgctactac 16012  
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OY 16013 aacctcggcctccaggttcaagcactctcctgctgagcctcagagtgctgagact 16072  
Db 41071 ATGTGGTGTCATTAATTAATCCGAGAAATTTGTGAATGATATCTTCCCATTTAT 41130  
OY 16073 acaagtcgcacacatagccagctaatcttgctgctgctgcttcttcttcttcttctt 16132  
Db 41131 ATTTTGTCTTCTTGTGTAAGATCAGTTGGCTGTAGATTTTGGCTTATTTCTGGGTT 41190  
OY 16133 agggcttcaac--atgttgccaggaatgctgactccttgacacttgatccaccac 16190  
Db 41191 GTCTATATGCTATTTGTTCTATATGCTTATGTTTATACATACATACATGCTTTTGGGA 41250  
OY 16191 ctggtccctcccaagtgctggaattacagcgtagagccacacacccggccttcttctt 16250  
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OY 16251 ttgtatttgtagctattgtaagtgagattgcttctgattggattcttcttcttcttctt 16310  
Db 41310 TTGCTTATGCTTGTGCTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 41369  
OY 16311 atatactgctgtagaagcaactactaatcttgatctgctgcttcttcttcttcttctt 16370  
Db 41370 TTTTCTAGTCTGTGAAGATGATGCTGTTTCTTTTAAATAGAAATTCACACTGAA 41429

OY 16371 actgattcatttaccacatctaagggttttttttttttttttttttttttttttttttttt 16430  
Db 41430 TTTGATGCTGTCATTTTCTCAGTATGCTGTTTACATATATGATTC--TATCA 41486  
OY 16431 tctctgctccagcctgtagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 16490  
Db 41487 TCCGTAATGTGGGATATGCTCTCATTGTTGTGTCTATATATGCTCTTCCAGCATG 41546  
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Db 41547 TTTTGTAGTCTGCTGTGAGAGATCTTTATATCTTGTGATGATTCCTAAGTATA 41606  
OY 16551 accaaccggcctaatttttgatttgatttgataggaagcgggttccacatttgccagc 16610  
Db 41607 TATATATATATATTTTCTTACACTATCTGAAGATGTTGAGTCTTGTATGATTCCT 41666  
OY 16611 tggcttgtaactagcactcagtgatctgagccactcagccctcccaagtgctggat 16670  
Db 41667 CAGCTGTGCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 41726  
OY 16671 taaggtcagtagcactcagcctgagcaactaagagtttgtaggagtgctttaggt 16730  
Db 41727 TGAATCTTCTGATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 41786  
OY 16731 ttctagataagataatcactcaggaagcaggaaggaattgactcctcttataa 16790  
Db 41787 TTTTACGAT 41846  
OY 16791 ttctgactccttcttctcctcctcctcctcctcctcctcctcctcctcctcctcctc 16850  
Db 41847 TTTGATGCTATATATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 41906  
OY 16851 taatgaag--agtgtgaaagtaggaactcctgcttctcctcctcctcctcctcctc 16906  
Db 41907 CGTTGAATGAGAGAGGCTGAAGTGGGATCCTTCTGTTCCAGTCTCCAGGGGATG 41966  
OY 16907 ctctcatcttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 16966  
Db 41967 CTTCATCTCTTCCCATCTGACATAGTGTGGCTGTGGGTTGTGATGATGCTC-- 42023  
OY 16967 ttatttgagtagatcttctcctcctcctcctcctcctcctcctcctcctcctcctc 17026  
Db 42023 ----TGAAGATGCTGCTCTCTATGCTGATTTGCTGAGAGTTTATATCAATAAG-- 42075  
OY 17027 gctgaatttaataatcttcttctcctcctcctcctcctcctcctcctcctcctc 17086  
Db 42075 ----ATTTGTCAAGCCTTTCTGCTATGATGATGATGATGATGATGATGATG 42127  
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Db 42128 TAAATCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 42187  
OY 17147 ttcttgtagataaaccacatgtagatgtagtatacttcttcttcttcttcttcttctt 17206  
Db 42188 TCCCTGATATAAACCACTTAATCATGATGATGATGATGATGATGATGATGATGATG 42247  
OY 17207 ggttctgtagatcttgtagagaatttgcatcttggttcaataatcctgattctt 17266  
Db 42248 GGTTCGAGATATTTGTGAGATTTTGTGATCTATGATGATGATGATGATGATGATG 42302  
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OY 17327 cttagaataagtagtaggagagcctgctc--cttgatttttggaatgcttcaagag 17383  
Db 42363 TTCAATAGATAGTATGAGAGATTCCTCTTTTATCTTTTGTGATATCTGTGATAG 42422  
OY 17384 tatgataactcctcctcctgtagatcttgtagaattcgctgtagcactcctgtag 17443  
Db 42423 GATTGTATCAATTTCTTTCAATGATGATGATGATGATGATGATGATGATGATGATG 42482



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repeat_region /note="LM1C repeat: matches 6. .466 of consensus"
8882. .9034
misc_feature /note="MIR repeat: matches 61. .218 of consensus"
join(9084. .9456,9534. .9640)
repeat_region /note="match: GSS: Em:A0079319"
9457. .9533
repeat_region /note="MIR repeat: matches 109. .184 of consensus"
9641. .9935
repeat_region /note="AluSx repeat: matches 1. .298 of consensus"
17482. .17548
repeat_region /note="MIR repeat: matches 184. .254 of consensus"
18491. .18567
repeat_region /note="MIR repeat: matches 63. .139 of consensus"
21277. .21497
repeat_region /note="MIR repeat: matches 12. .241 of consensus"
22549. .22838
repeat_region /note="AluSx repeat: matches 1. .311 of consensus"
23004. .23323
repeat_region /note="AluSx repeat: matches 1. .304 of consensus"
complement(23633. .23767)
misc_feature /note="match: GSS: Em:B54082"
23768. .24006
repeat_region /note="MIR repeat: matches 34. .262 of consensus"
24007. .24275
repeat_region /note="match: GSS: Em:A0084181"
24500. .24808
repeat_region /note="AluSg repeat: matches 1. .308 of consensus"
24928. .25259
misc_feature /note="match: GSS: Em:A0020936"
25260. .25401
repeat_region /note="MIR repeat: matches 8. .148 of consensus"
26371. .26581
repeat_region /note="MIR repeat: matches 24. .259 of consensus"
27025. .27330
repeat_region /note="153 copies 2 mer tt 55% conserved"
27162. .27401
repeat_region /note="5 copies 48 mer 64% conserved"
28156. .28667
repeat_region /note="LM5C repeat: matches 1589. .2095 of consensus"
28725. .28814
repeat_region /note="LM1D repeat: matches 416. .505 of consensus"
28965. .29499
repeat_region /note="LM5C repeat: matches 986. .1533 of consensus"
29817. .30204
repeat_region /note="LM1A10 repeat: matches 5776. .6165 of consensus"
30215. .30479
repeat_region /note="LM1A10 repeat: matches 5476. .5748 of consensus"
30499. .30719
repeat_region /note="LM1A7 repeat: matches 5920. .6138 of consensus"
31881. .32026
repeat_region /note="73 copies 2 mer tt 72% conserved"
31887. .32030
repeat_region /note="3 copies 48 mer 81% conserved"
31959. .32026
repeat_region /note="17 copies 4 mer tt 84% conserved"
32571. .32692
repeat_region /note="LM1A15 repeat: matches 6035. .6157 of consensus"
32883. .32943
repeat_region /note="LM2 repeat: matches 2688. .2748 of consensus"
33321. .34232
repeat_region /note="LM1A16 repeat: matches 57. .356 of consensus"
complement(34750. .34876)
misc_feature /note="match: GSS: Em:A0037163"
36994. .37059
repeat_region /note="LM2 repeat: matches 2642. .2709 of consensus"
37933. .38313
misc_feature /note="match: GSS: Em:A0147783"
38406. .39036
repeat_region /note="LM2 repeat: matches 1976. .2618 of consensus"
39844. .40115
repeat_region /note="LM13 repeat: matches 2958. .3226 of consensus"
40116. .40405
repeat_region /note="AluSx repeat: matches 1. .290 of consensus"

repeat_region 40406. .40794
repeat_region /note="LM13 repeat: matches 3226. .3624 of consensus"
40811. .42269
repeat_region /note="LM1B3 repeat: matches 4690. .6150 of consensus"
42275. .44271
repeat_region /note="LM13 repeat: matches 3611. .5616 of consensus"
44272. .44530
repeat_region /note="LM12 repeat: matches -448. .191 of consensus"
44560. .44571
repeat_region /note="LM1B2 repeat: matches 5096. .5915 of consensus"
45368. .45520
repeat_region /note="LM12 repeat: matches 592. .744 of consensus"
45529. .45753
repeat_region /note="LM1B2 repeat: matches 5923. .6155 of consensus"
45768. .45921
repeat_region /note="MER45 repeat: matches 3. .1039 of consensus"
46235. .48387
repeat_region /note="LM12 repeat: matches 63. .2215 of consensus"
48388. .48693
repeat_region /note="Alu1b repeat: matches 1. .301 of consensus"
48694. .50660
repeat_region /note="LM12 repeat: matches 2215. .4144 of consensus"
50661. .51079
repeat_region /note="LM1A11 repeat: matches 5741. .6165 of consensus"
51080. .52340
repeat_region /note="LM12 repeat: matches 4143. .5403 of consensus"
53087. .53454
repeat_region /note="THE1C repeat: matches 1. .371 of consensus"
54345. .54599
misc_feature /note="match: STR: Em:G02936"
complement(55044. .55243)
misc_feature /note="match: 278774 chromosome 6 HindIII fragment"
55715. .55754
repeat_region /note="20 copies 2 mer ca 90% conserved"
55917. .56008
repeat_region /note="LM1B3 repeat: matches 6035. .6130 of consensus"
56349. .56546
repeat_region /note="MIR repeat: matches 2. .211 of consensus"
57477. .57788
repeat_region /note="Alu1b repeat: matches 1. .310 of consensus"
57822. .57920
repeat_region /note="LM1 repeat: matches 1. .99 of consensus"
57918. .62937
repeat_region /note="LM1A2 repeat: matches 1094. .6146 of consensus"
63160. .63293
repeat_region /note="MIR repeat: matches 120. .245 of consensus"
63893. .63928
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67203. .67344
repeat_region /note="71 copies 2 mer gt 75% conserved"
67203. .67342
repeat_region /note="35 copies 4 mer gtgt 74% conserved"
67248. .67343
repeat_region /note="2 copies 48 mer 90% conserved"
68668. .68788
repeat_region /note="FRAM repeat: matches 1. .133 of consensus"
68794. .69028
repeat_region /note="LM1A16 repeat: matches 5921. .6157 of consensus"
69242. .69453
repeat_region /note="MIR repeat: matches 3. .237 of consensus"
complement(69687. .69961)
misc_feature /note="match: GSS: Em:A0206943"
69962. .70098
repeat_region /note="MIR repeat: matches 40. .185 of consensus"
70124. .70649
misc_feature /note="match: GSS: Em:A0380554"
71206. .71716
repeat_region /note="LM2 repeat: matches 2194. .2748 of consensus"

Query Match 6.5% Score 1222.8; DB 11; Length 104594;
Best Local Similarity 63.8%; Pred. NO. 1e-191;
Matches 2710; Conservative 0; Mismatches 1052; Indels 486; Gaps 37;
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QY	14621	tggtatataatacccaatttcttctaactgttcatccaattgataagcaactaagttgaatt	14660
Db	92356	TATAATATATATAACATTCTTTTATCCACACAGTATGATGAGGCAATTGGCGTGGTT	92297
QY	14681	ccatatcttgcgtgtgtaagtagtgcgcgaataacatacgcgtgcacatactcttag	14740
Db	92296	CCATATTTTTCGAATTGGCAATTGGCTGCTGCTTAACATGCATGTGCAAGTACGTTT	92237
QY	14741	ataataaattct- tttcttttgtaaaaactagtagtggagttgtcagaatggaaaga	14799
Db	92236	GTAATATGATATCTATTCCTGTGGTAGATACCACTACATGAGGGGTGCTGATCAATAGG	92177
QY	14800	tagtctatatttaattctcttggagaagaaactccatactgtttccataagagcgtgaactaa	14859
Db	92176	TAGATCTACTTTTAATTCTTTTAGAANAATCCACACTGTTTTCCATAGGGTTGACTAG	92117
QY	14860	tttaattccccaacatggtatataaagatccctttttcacatgataaccaactg	14919
Db	92116	TTTAATTTCCACCGAGTAGTGTAAAGATATTCCTTTTCACCATATCCACACCGACA-TC	92058
QY	14920	tctgtcttttaataaaagacattctgcataagataagtgatactatcttggaaattg	14979
Db	92057	TATATTTTATGATATGAGCCACTGTGACAGGTGAAGGTGATATGATCATATGTTTGG	91998
QY	14980	attgcattctccctatgactgtaagtgttggaatttttcataactgttgg-----	15035
Db	91997	ATTTCATTTCCAGTATCATTTGTGATGTGAAACCTTTTTTTCAGCTTTGTTGGCCATT	91938
QY	15035	---ggtatgccttggaaaaagtcatactcatgigtgttgccatacttttaataagatg	15091
Db	91937	TGTGATCTCTCTTTGAGAAATGGCTATTAATGCTTAGCCCACTTTTGTATGGGAATG	91878
QY	15092	ttagatttttttggtttggaaatcgttttagtctcgtgtgtagctgataatagtcgcc	15151
Db	91877	-----TTTTTTTCTGTGCGATTTGTTTGAAGTCTTGTGAATTCGTGATATTAATCTCT	91823
QY	15152	tggtgatagaataatttgcagaataattctcgtcatcaacaagatgtgtctctcaa	15211
Db	91822	TGTCAAGTACACAGATTGTGAAGATTTTTTCCCACTCGTAGG-TGGCTGTGTTACTGTG	91764
QY	15212	tctgtattcttcttggcatgagaagacttttaattgaatgccatttg-----	15267
Db	91763	CTGATGTGTTCTCTTGCTGCTGAGAGAGC-TTTTAACTTAATTAAGTACCATCTATTATATC	91705
QY	15267	-----	15267
Db	91704	TTTGTTTTCTTGCAATTGCTTTTGGGTCTTGGCATATAAAATCTTGTGCTAAGCAATG	91645
QY	15267	-----ctgtttctcagtaacttatataagttt- gggcttacaact	15304
Db	91644	TCTAGAGAGGGTTTCCATATGTTATCTCTAGAAATTTTATGTTTTCAGGCTTAGAATT	91585
QY	15305	taagctcttaataccaaccttgagttgaattttatcgtatcagtgagaagataaagaagttcaatt	15364
Db	91584	TAAAGCTTTGAACCAATTATTAATTATTTTGTTTAAG-GTGAGAGAGAGAGATCCAGTT	91526
QY	15365	gaactctctgataatgataatcaattttccagcacacatgatgtaagaaggtttggt	15424
Db	91525	TC-TAATTCATCTTGTGGCTTCCAAATTAATCCACACACCAATTTGTTAAAAAGGGTCTCT	91467
QY	15425	tccaacagtgatgtctctgtgtcgcgttgtgcaaaaatcagttgagtcgaagtatcggt	15484
Db	91466	TTCGCCACATTATGTTTTTGTGTTGGTTGTCAAAATATAGTTGGCTGTAAAGATTTGGCT	91407
QY	15485	ttaattctggagctctcctatgctggttccaattgaaactggtgtgtctatttttaacagtaa	15544
Db	91406	TTAATTTGGGGTTCATCTATCTGTTCCATATGTCATATGG-CCATTTTAAATATAGTAC	91348
QY	15545	cctgtgtctcgttgtaagtaatgcttgtaataaattggaagtgaataatgtatgct	15604
Db	91347	CATGCTGTTTGTGTACTATACCTTTAATAGTATTTGAAGTGTGGTAATGTATGCTCT	91288
QY	15605	ctagcttaattcttcttgcagaactgcttgagctatgggactcttttggttcat	15664

Db	91287	CCAGATTTGTTCTTTTGGCTTAGATTTCTTTGGCTCTGTGGCTT-TTTTGGTTCAAT	912239
Qy	15665	atgaaatttagagattgtttttcttaattctgcacaaataactctgtgtaattttgtaggg	157244
Db	91228	ATGAATTTTAGAAT-TTTTTCTAGTCTGTGGATAATGATAGATGATTTTGTATGGGA	911707
Qy	15725	attctatagaataatgtaggcctcttctgtacagtagtcatctttaatgatattctctcga	157844
Db	91169	ATTGCAATTAAATTTGTAGATCACTTTTGGAAATATGGTCAATTTTACCAATTTGATTCGA	911100
Qy	15785	atatacagtagcacaggaatgttttccattgtgtcagtataatttctttagctcgtg	158444
Db	91109	CTCTCCATGACATGAGGATGATTTCCAT------	910787
Qy	15845	tttttagtctcccttgtaggaatttaacctgtgttaataataattcctagttgtgtg	159044
Db	91078	-----AGTTT	910744
Qy	15905	gtgtgatagtgtgtttataaattccttttcttttcttttcttttcttttgagcagagctc	159644
Db	91073	GTTGGTTTATGATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGAGGAGTCTC	910144
Qy	15965	actctgtaccccaaggctgagagcagatgagacaaactctgcgtactataaacctccggctc	160244
Db	91013	GCTCTGTGCCCGAGCTGAGTGCATGGCGGGATCTCGCTCACTGCATGCTCCGCTTC	909544
Qy	16025	ccaagttcaagaactctctctccctgcagcctccagaatgacgtgaggaactacaagtgcac	160844
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Qy	16085	cactatgcccaactaaatttgtgtgtgtgtatttttagtagagacaaggtttcacca	161444
Db	90893	CACCTACCCCGGCTATTTT------TGTATTTTATGAGACGGGCTTTACCG	908434
Qy	16145	tgttggccaagatgtgtctcgaaattcttgaaactgtgtgataccaccactgtgcttcccaa	162044
Db	90842	TTTTAGCTGGGATGCTTCGATCTCTCGACCTCGATCCGATCCGCCGCTCCGCTCCAAA	907834
Qy	16205	gtgcgtgagtaacagagcttgagcaacaacaacccggcctttttctttgtattctgtagc	162644
Db	90782	GTGCTGGGATTCACAGCGTGAAGCCACCGCGCCGCTATGATTTCTTTTACAGATGTTT	907233
Qy	16265	tattgtaaatggaatgtgtctcttgaattgtgtttcaatttgaatcatattgtgtgtga	163244
Db	90722	TCTAGT-----TTTCTGTGAGAGTCTTACACCTCCTTGTTAGGAATATTC	906744
Qy	16325	gaacaactaataatttctgtagtgtgattgtatcttgcaagtttaactgaattcaatta	163844
Db	90673	TATATATTATTGATTTTAAATTTTAAATTTTATTTTGTGGCACTTATTTGTAAT	906200
Qy	16385	ccaatctcaaggtttttttttttttttttttttttttagaacaagaattcatctcgttgccag	164444
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Qy	16445	ctgagatgcaatgycacaactctcaagctcagctcagctcgtcccggttcaagtat	165044
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Qy	16565	attttttagatttttagtagagacaggtttcaacatgtttggccaagctgtgtctgaacac	166244
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Qy	16625	tgaactcaagtgatctgccaactcagcctcccaagtgctggaattacaagcatgaagct	166844
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 QY 16865 ga-----aagtaggcacccctgttcttccacagcttct 16897  
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 QY 17729 atcaatttcttatacttcttgaagaaacagccttcttcttcttcttcttcttcttcttct 17788  
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QY 17789 ttttttcatcatatatttcatattagttctgcctgcatct--tattcttcttctct 17845  
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 QY 17906 attacttgaatc-ttctctcttcttgaatgaatgaatgaatgaatgaatgaatgaatgaat 17961  
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 QY 18322 gttcaatttgcttcaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 18381  
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 QY 18619 gccattttaggattcacttcttcaatgcttcaatgcttcaatgcttcaatgcttcaatgct 18678  
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RESULT 10  
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 DEFINITION Homo sapiens chromosome 4 clone B341C20 map 4q25, complete  
 sequence.  
 AC004704  
 ACCESSION AC004704  
 VERSION AC004704.2 GI:4417258







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Oy	16091	gcccgcgaatttttctgtgtgtgtatcttttagtaagacaggtttcacatgttg	16150
Db	96074	GCCCGCAATTTT-----TGTAATCTTAGAGATGGGGTTTCTCAATCTTG	96123
Oy	16151	ccagatgtctcgcgtctcttgacctgtgtaccacccaccttgccctcccaagtctg	16210
Db	96124	CCAGCT-----GAGCTCTGCACATCGGATCCACCCACCTCCACCAAGTGCTG	96177
Oy	16211	ggattacagcgctgagccacacacccgccttttttttctgtattgtgacctgtg	16270
Db	96178	GGATTACAGGGGTGAGCCACCGCGCTGGCCCAAGATTGTTTTCTAAT--CTGTGA	96235
Oy	16271	aaatggattgtgtctctgattgtgttcaatttgaatcatatgtgtgtagaaca	16330
Db	96236	GAATTAGTGGTATTTTCATATGGGGGATTTCATTAATTTAGATAGCTTTGGCAGTA	96295
Oy	16331	ctaccaattctgtatctgattctgtatctctgcagaattactgaattacatccaat	16390
Db	96296	TGGTATTTTCACATATTGA--TTCACACTCATAGCATAGCATGGGATGTGTTCATT	96353
Oy	16391	ctaaggcttt	16450
Db	96354	GTTCAATGACATAGATTCTTTCAGCAGAGTTTATTAGTTTCTT-----TGTAG	96405
Oy	16451	tgcgaatgcacaaatctcagctcagctcagctcctcccggttcaagtctctct	16510
Db	96406	AGGCTTCTATTTCTTGTTGGTATATTCCTATTATTATTATTATTATT-----	96461
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Db	96461	-----GCACCTAAT	96469
Oy	16571	gtagtttagtagagacagggttccacctgtgccaagctgtgttgaactacagact	16630
Db	96470	GTAATATGGTAGAATTTCTTGATTGTGATTCCTCGTTGGTGTCTGTGGTGA-----	96523
Oy	16631	caggtgacctgcgcacccctccacccccaagtgcctgggaattacaggaatgacctacgcg	16690
Db	96523	TAGAGACTACTGATTTGTATATTTATATCTGTATACCAAGAACTTTGTGCAATTTT	96582
Oy	16691	ccctggcaaatctaagagttttgtgtggagtccttaagttttctagatataagcata	16750
Db	96583	TTTATCACTTTAGCGCACTTCTCGAGGAATCCTTAGGGTTTCAAGGAACGATCATTA	96642
Oy	16751	tcatcaggaacacaggaataattgtacctcttccttatattgaattgacctgtttca	16810
Db	96643	TCGTCAGCAACAGTGGCAGTTGCTCC-TCCTTACCAATGTGATGCCCTTTATTCA	96701
Oy	16811	ttctcttccttgatgtcctgtgttaggaattccaactatataatga--gagtgtgaa	16867
Db	96702	TTCTCTTGATGTGCTGACCTGGCTGAGCACTTCCACTATCTTGAAGAGAGTGTGAG	96761
Oy	16868	agtaggaatcctgttttctccagttctta-aaggaatgcttcatctttccctatc	16926
Db	96762	AGTGACATCTCTTGCTTTGTTCACATTTCTCAGAGGAATGATTTCAATTTTCCCATTC	96821
Oy	16927	agtaagatgttagttacaggtttacacataatgacctatatttgagtgatgact	16986
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Oy	16987	tctgtgctagtcttaacaaaggttttctcttaagaaaggaatgtgaattatataactc	17046
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Db	96942	TTTTCTGCATCATTAAGATGTCTATGATTTTGTTTTAACTGTATTATGTGGTGT	97001

QY	17107	atcaaatattatgattgaaatcgtttaccctccttgatcccggtgaataaacccact	171566
Dd	97002	atccactttattttagacctgtaattgttaaacctaccctcgactctgtatattgaaccact	97061
QY	17167	tgaatcagtgatcatcattctttgatcttggttgattggtcttgatgattttggtg	17236
Dd	97062	tcattcatggtgatattatcttttttgatattgtttgatttggttgactgtattttgtta	97121
QY	17227	aggattttgcattctgtgttcaatcactcgtatggtttctcttattctgtatcccttgtt	17286
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QY	17287	ttgttcctctcttggtttttgtatcacaggagaaatgagccctatagaataagttagga	17346
Dd	97177	ttttgtctcttttcttactggttttgatttttagggctatctgctctcatagaattgaattagga	97233
QY	17347	gaagcctgtcctt---gatttttggaaagtctcaagagattatgatatctctctt	17403
Dd	97237	gggttccttcttcttctgtctgtctgtggaaatagggtcaaaagaaattggtaccattcttctt	97296
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Dd	97297	tcaaatatctggagaaattctgcgtgaaactctgcgcttcctgacttttggtgtgttg	97356
QY	17464	gattgaaaatattactgattatcttgctgcattatgttgcattatgctatagaatttcgt	17523
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QY	17697	ctctcttcttggttagctcgtgaagtggtttatcaattcttcttatactccttgaagaac	17756
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Dd	97657	cagctttttttttttgtttcattttatctttttgtttttttttttgtttgttttcaattttcat	97716
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QY	17928	ttttgatgaaatttattctgtctg---ttctctttagcacctcgtcttgcttgatccc	17983
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QY	18104	tattctgtaaggttgtaaattctctctcgtgatattcttcagatttatactcgcgtgt	18163
Dd	98014	tattttcattggctttgaagggttcttttgagattttatccagtttttatccactgtat	98073
QY	18164	ctgagaaagcactgtagtgaatttcagttttaaaaaatttglttgacctgtgtttgtg	18223

Db	98074	CTGAGAGAGTCTGTGATATTAATTTCAAATTTCTTTAATTATTGGGGC-TCATCTTAATGG	98132
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Db	98133	CCTATCATGTGGCTATCTCCGGAGAAAGTCCATGTCCTTTGAATAAATGCTATTCT	98192
Qy	18284	gcagttgtctgataagaaatgtttgttaaatgtctgtaagtcatttgcgtctaaagtcag	18343
Db	98193	GCAGTTGTGGATGAATATGTTCTGTATACATCTGTAAAGCCATTGGTCCAAAGTATAG	98252
Qy	18344	tttaagtcgaagttctctctctgtcatctcttgcctagatcatctgtctaatctgcgtaat	18403
Db	98253	TTTAAACCATGTTCTTCTGTGACATTTCTGCTGATACCTGTTAATGCTGTAGT	98312
Qy	18404	gggggtgtaattctcaacatatgtgtgcagtgatctctctctcttaagtcagtaaat	18463
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Qy	18464	actgtttctatgacctctagtactccagtgctgggtgcaataatgtattagaattgta	18523
Db	98372	AATTTGTTTATAAATTGGGAGGCCAGCTGTAGGTC--AATGATGTTTAGTATTGTGA	98429
Qy	18524	tatatctctgcgaattgtctctttaataataataaagaactctcttagtcctttttt	18583
Db	98430	PATTTTCCGTGGAGAACACTCTTTTACCATTAATAAATGTCCTCTTTCACAGCTGTT	98489
Qy	18584	tttttttaactgctttt 18600	
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RESULT	11			
LOCUS	AC008886/c			
DEFINITION	AC008886	94220 bp	DNA	HTG 03-AUG-1999
	Hom sapiens chromosome 5 clone C17B-H1-2219D10,			*** SEQUENCING IN
	PROGRESS ***	20 unordered pieces.		

ACCESSION	AC008886
VERSION	AC008886.1
KEYWORDS	HTG; HTGS_PHA8E1.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 94220)
TITLE	DOE Joint Genome Institute.
JOURNAL	Sequencing of Human Chromosome 5
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 94220)
TITLE	DOE Joint Genome Institute.
JOURNAL	Direct Submission
COMMENT	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA www.jgi.doe.gov.

```
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*	1	719:	contig of 719 bp in length
*			gap of unknown length
*	720	1561:	contig of 842 bp in length
*			gap of unknown length
*	1562	2552:	contig of 991 bp in length
*			gap of unknown length
*	2553	4021:	contig of 1469 bp in length
*			gap of unknown length
*	4022	6364:	contig of 2343 bp in length
*			gap of unknown length
*	6365	7026:	contig of 662 bp in length

Query Match	Best Local Similarity	Score	DB	Length
Matches 2733; Conservative	63.4%	1201.2;	DB 41;	94220;
	0;	Pred. No. 3,7e-188;	Mismatches 1243;	Indels 336; Gaps 45;
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Db 65030	GATTTCATTCTTTTTCATGGGTGAATACATTTCATTATGATATATACCACTTTTCTT	64971		
Oy 14645	tactgttcattccatttgtagacactgaattgatttcatactcttgctgttgaaatag	14704		
Db 64970	TATCATTTAGTGCACATGATGAAACCTTAGTGTGATTCATATTTTGGCTATACGAATAG	64911		
Oy 14705	tgctgcagtaaacataactcgtgtgacacatctctttagataataattcttcttctt-t	14763		
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Oy 14884	aagagttcccttcttctt-----cacatagataaccaaatgtctgtcttcttataataa	14937		
Db 64730	AGGGTTCCTCTTCTCTGCAATCTCACACGATCATTAATGCTTACTTTTGTATATA	64671		
Oy 14938	gacattcgcattagataagtgatatctatcttgtaattgattgattgcattctctta	14997		
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Oy 14998	actggtaatgttgagcatttttccataaccctgttg-----gtatgactttgaa	15049		
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D6	62407	CATATATGGCCCTTATTTATTTGTTATATATATTCATCTTAATCCATCTTAATCCCATTTTGAATGAGGCGCT	62348
OY	17012	ttcttaagaaggagatcgtgaatcttatttaaatctcttcttcgcgtccataaagatgatca	17071
D6	62347	T--TAATACAGAAAGTTTAAATTTATATCAAA--TGTTTCTGGCAGCTAATGAAATACCA	62291
OY	17072	tatggttttgcctccatctcgttgatataatgatatcaattatcttatgattgattgatagt	17131
D6	62290	TTGTGGCTTTTGTCTTGCTTGTTATGTATGTATGTATTAATGCTTAATTAATTTGCTTAAT	62231
OY	17132	tgacctatccctgcatactccctgtataaaacccactgcatacgtgtatcatctcttga	17191
D6	62230	TCACACATCCTTGCAATCCCTGGAGATGAATCCCTCTTGTCAGATGGATGATATTTTAA	62171
OY	17192	tttgatgttgagatcttggtttctagatattctgtgaagatctttgcattgtgtcaata	17251
D6	62170	TTGATGGTTAAATTCAGTTGTATGATATTTGTTGGAATTTTTCATCTATAGTTTATCA	62111
OY	17252	atccgtatgttctcttttcttctatcccttgatcccttggttgcctctctgtgtgttctat	17311
D6	62110	--CTGATATTTGGCCCTGTAGTTTCTTTTGTGTGTGTGTGTCTCCCTGCTGTTTGGCAT	62053
OY	17312	caaggcgataatgcgtcttataagaataagtaagggaaggcgctccctcgtatttttggaa	17371
D6	62052	CAGAGTAATTTCTGATCTGTATGGGAGATTTGAAGATATTTCTCTTAATCAATTTTTT	61993
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Qy	18127	ctcttgcattgattccattcagtttattcttcgtgtgtgtctgcagaagcactgattgatt	18186
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DEFINITION	Human Chromosome 11 pac pBJ392a17, complete sequence.		
ACCESSION	AC000385		
VERSION	AC000385.1		
KEYWORDS	HTG.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 165491) Evans,G.A., Athanaslou,M., Basile,M., Bradbury,P., Brignac,S., Bumesler,R., Davis,C., English,C., Franklin,T.L., Garner,H.R., Gee,V., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U., Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S., Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D., Ward,T. and Wilson,R.		
TITLE	template		
JOURNAL	unpublished		
REFERENCE	2 (bases 1 to 165491) Evans,G.A., Bradbury,P., Brignac,S., Bumesler,R., Burpee,D., Davis,J., Davies,C.J., Davis,C., English,C., Fondon,T., Franklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U., Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S., Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D., Ward,T. and Wilson,R.		
AUTHORS	Direct Submission		
TITLE	Submitted (04-APR-1997) Genome Science and Technology Center, University of Texas Southwest Medical Center at Dallas, 5323 Harry Hines Blvd, Dallas, TX 75355-8591, USA		
JOURNAL	3 (bases 1 to 165491)		
REFERENCE	Evans,G.A., Athanaslou,M., Basile,M., Bradbury,P., Brignac,S.,		





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Oy	18594	cgttttttagacgtgtttttcccttcgcacatttttagaacctcctcaacttgactta	18653
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RESULT	13		
LOCUS	HSL196A2		PRI
DEFINITION	Human DNA sequence from cosmid 196A2, Huntington's Disease Region, chromosome 4p16.3, containing multiple EST matches defining gene fragments and 2 CpG islands.		
ACCESSION	Z68165		
VERSION	Z68165.1 GI:1107693		
KEYWORDS	4p16.3; CpG island; Gene fragment.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 35281)		
JOURNAL	Williamson,H.		
COMMENT	Direct Submission Submitted (04-DEC-1995) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail enquiries: humpub@sanger.ac.uk IMPORTANT: The true left end of clone L96A2 is at 1 in this sequence. The true left end of clone L19H1 is at 35182 in this sequence. The true right end of clone L27H9 is at 8050. The start of this sequence overlaps with the end of clone L27H9. This sequence is not the entire insert of clone L96A2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. L96A2 is from cosmid library LA04NCO1 constructed at the Human Genome Center, Los Alamos National Laboratory, NM 87545 under the auspices of the U.S. Department of Energy. The library was constructed using flow-sorted human chromosome 4 from a Hamster-Human hybrid cell line (UV20HL21-27) containing human chromosomes 4, 8 and 21. VECTOR: scos+1 L96A2 is contained in a clone contig spanning 2M which is described in Baxendale et al, Nature Genetics 4 (1993) ) 181-186. See also Myers et al, Cytogenet Cell Genet. 66 (1994 ) 218-230. Location/Qualifiers 1..35281 /organism="Homo sapiens" /db_xref="taxon:9606"		

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DEFINITION	Homo sapiens BAC clone RG242D01 from 7q11.2-q21, complete sequence.		
ACCESSION	AC002068		
VERSION	AC002068.1	GI:2076719	
KEYWORDS	HTG.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 58645)		
JOURNAL	Magdi, L., Goela, D., and Harper, M.		
REFERENCE	Unpublished (1998)		
AUTHORS	2 (bases 1 to 58645)		
JOURNAL	Waterston, R.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (09-MAY-1997) Department of Genetics, Washington		
TITLE	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA		
JOURNAL	3 (bases 1 to 58645)		
REFERENCE	Waterston, R.		
AUTHORS	Direct Submission		
TITLE	Submitted (24-SEP-1998) Department of Genetics, Washington		
JOURNAL	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA		
COMMENT	SUBMITTED BY: WUGSC		
	Genome Sequencing Center		
	Department of Genetics		
	Washington University		
	St. Louis MO 63108, USA		
	http://genome.wustl.edu/gsc		
	mailto:sapiens@watson.wustl.edu		

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPING INFORMATION:  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NRCRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center.

For additional information about the map position of this sequence see <http://www.nhgri.nih.gov/DIR/CTB/CHR7> or <mailto:egreen@nhgri.nih.gov>

The sequen of this clone was established as part of a mapping and sequencing collaboration between the NIGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GTB/CHR7> or <mailto:egreen@nhgri.nih.gov>

**SOURCE INFORMATION:**  
clone RG342201 is from a release of the human BAC library  
CIRB-HS-A. The library contains cloned DNA from human sperm. See  
Shiuya et al., *Proc. Natl. Acad. Sci. USA* 89:8784-7 (1992).  
Kim et al., *Genomics* 34:213-8 (1996). The clone is available from  
Research Genetics, Inc. (<http://www.rsgen.com>).  
**VECTOR:** pBeltoBAC11

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RG290G13, 199 bp overlap; the clone sequenced to the right is RG333F24, 200 bp overlap. Actual start of this clone is at base position 1 of RG242D01; actual end is at 22809 of RG333F24.

This clone contains a polymorphic base (an extra A) with it's left neighbor RG290G13 at base position 4337.

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QY 13940 ttaagatgattttatttatttatttacttttatttctgttacaactt---tatgggtacat 13995
DB 15260 TGGGGATTACATTAGATCTTTAAACCATTTTGAGTTGATTTTGGCATTAAGTAAAGAA 15319
QY 13996 atgcagtttctgtaacagcatagattatgctgcagcaagtggaggtctttaaggtatcc 14055
DB 15320 ATGGAGGCTCTCTTCATCTTCTTGCAATATGATATCAAGAGTGTCCAGAAACAATTAAG 15379
QY 14056 atcaactgaataaggttccttgctccatgaagaatttccatccatccctccacctcct 14115
DB 15380 AGGGTGT-ACTTTCTTAGTGTGATATACTTGACACCTTTGTGCAAAAGTTAGTTGGCTTGA 15388
QY 14116 cattcttccactcattatgtatcatccactcgtcatctgtytgaacaagttgttttag 14175
DB 15439 GCTATGTAATTACTCTCTGGGTTCTTTATTTTGTTCATTAATCTTGTTTCTGTTT 15498
QY 14176 aacacactatgagtcgaagaacataactgctcttctgtgcccgtgttctttaacctaa 14235

```





Db	19833	GTATGATGAGCTATCCAAATTCCTGAAGATGTGGGGGGGTGAAGTTCCTATTACGTTT	19882
Oy	18432	tgcagctgatactcttctttagtctagtgaaactggtttatagctcttagtaactcag	18431
Db	19883	TGTGGCACACCATCTCTTTAATCCAGTAGATTACTCTTAAATGTGGACCTGCCAA	19942
Oy	18432	tgtcgggtgcaaatatgtaatttagaagtgtataatactctgcgaatggtctcttaa	18551
Db	19943	TGTTTGAAATCAATATAT-----AATATATATATCTCTATCTGAAATGATGCCATTAT	19994
Oy	18552	tattataaacgaacttcttagtctcttttttttttttttaacigtcttttagatggttt	18611
Db	19995	TATTTACAAATCTCTTTTGTCTCTTTTAAATTTTGGACTAGTCGTGTTTAGTATA	20054
Oy	18612	tctctctgcacattt	18626
Db	20055	GCTACTTTTGCTCTT	20069

RESULT	15
AC009408/c	
LOCUS	AC009408/c
DEFINITION	AC009408 171212 bp DNA HTG 25-SEP-1999 Homo sapiens clone NH0227718, *** SEQUENCING IN PROGRESS ***, 3
ACCESSION	AC009408
VERSION	AC009408.2 GI:5923732
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo. 1 (bases 1 to 171212)
AUTHORS	Waterston,R.H.
TITLE	The sequence of Homo sapiens clone
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 171212)
AUTHORS	Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (21-AUG-1999) Genome Sequencing Center, Washington

**COMMENT**

On Sep 25, 1999 this sequence version replaced g1:5575730.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 3 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of 'N', but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1	3801:	contig of 3801 bp in length
3802	3819:	gap of unknown length
3820	33560:	contig of 29541 bp in length
33561	33378:	gap of unknown length
33379	171212:	contig of 137854 bp in length.

FEATURES	Location/Qualifiers
source	1. .171212

BASE COUNT	47079	a	37780	c	38895	g	47332	t	36	others
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="NH022711"									

Query Match	6.3%	Score 1175:	DB 41:	Length 171212:
Best Local Similarly	67.0%	Prog. No. 7.4e	184:	
Matches 2293:	Conservative	0:	Mismatches 930:	Indels 200: Gaps 36:

Qy 15268 tgccttctagatccttatagtttggcgcttaacactaagtccttaatccaccttgagt 15327

QY	15328	tgattttaaagttaagtaagaagatcgaatgcatctctccgatatgagatc	15387
Db	46258	TGGTTTTGTATATG-GTAGAGAAATAGGCTTAATTATCTTCCAAAGTA---TCTT	46203
QY	15388	taattcttaagacacatgatattgaagaagggcttcgtttccacagtgatgctctgcg	15447
Db	46202	CAATTGGCCAGACACATTATTGAAAAAGCTGCTTCCCTAATATATGTTCTTGCGA	46144
QY	15448	gctttgcaaacatcagttgctgcgaagatgcggtcttattctcgtgtctctatgcg	15507
Db	46142	CTTTGTGTGAAATCA---GGTAGCAAAACGGTAGAATTATTTCTGGGTTCTCATCTG	46086
QY	15508	tccattgacctgctgtgctctattttataacagtaacctgcgtctcgtttagtaagt	15566
Db	46085	TTTATATGGCTATATG-----CCCTATTTTATAGCTAGTAGG	46045
QY	15568	ctgttaataaattgaattagaataatgtagtcgtcctagcttatctctttgtccag	15627
Db	46048	CTTTACAAATTTCTAAGTCAAGTAGAGTAGTGCCTCCACCTTTGTTCTTTGCTCAT	45988
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Db	45988	GATGCTCTTGGCATTCAGGC-TCCTGTGGTTCATACAAATTTTGGATGTTTTTTC	45930
QY	15688	taatttgcacaaataaactgtgtaattttgataaggatgtatagaaatgtaagctgc	15747
Db	45929	TATTTCTGTAAAGAAAGTCACTGCTATTTTATAAGATTTGCATTGAATCTGTAGATCA	45870
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QY	15949	tttgaagcagagctcaactctgtccaccaggctgtgagtgacgtgcaacaactcggctta	16008
Db	45631	TTTAAAGCAAAAGCTCACGTGTCCACAGGCTGAGAGTGAAGTGTATCTCCACTCA	45572
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QY	16129	agaagaggttttaccatgtgtgccaagatgtgtcctgatctctcttagacttgaatc-caac	16187
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Db	45400	TGCTCTGGCTCCCAAAAGTGTGGGATTTACAGGATGAGCCACCTGCTCCAGCCGTACT	45341
QY	16244	--ttttttttgtattgttagctatgttaaatgggattgtgtctctgattgttttca	16303
Db	45340	AAATTTTGTACATGATTTTGTATATTCACAATTTATGTGATTCATCGATCAAGTTCTAA	45281
QY	16302	ttttgaatcatattgtgtgtgagaacaactacaattttgtatgtgtatctgtatcct	16361
Db	45280	CAGTTTTTATAGTGAAGCTTTTAAAGATTTTAAATATGAGATCAAGTTGTTGCCAAAG	45221
QY	16362	tgcagtttactgaattcattaccacaactaag---ggtttttttttttttttt	16415



D	45220	GAAAGATTGATTTCTCTTTCACAAATTAGATGCCCTTTCTTTCTTTTTTTTTTT	45161
O	16416	TGAAGACAATtctatcctgctccaggtcggaagtgcacattcgacaatcagaactact	16475
D	45160	TGAGACGGAGTGCTCGCTGTCCGCCAGCGTGAAGTGAAGTGG - ACGATCTGGGCTACT	45102
O	16476	gcaagctctgctcccgggttaaatgatattccctgcgccagctcccgagtagctggga	16535
D	45101	GCACCTCCGCTCCCAAGGTTTACGGCATCTCCTCCAGCCTCTTAGAATCGGGGA	45042
O	16536	ttaaggagctgycaccacacacacgaactatttgtagtttagtagagacaggttc	16595
D	45041	CTACAGGTCGCCGCCAACCAATGCCCGCTAATTTTGTATTTAGTAGAGACGATTTTC	44982
O	16586	accatgttggcc- agctggtlcttgaactcgaacctgaagtgatctgcgaacctagcct	16654
D	44981	ACCAGTGTAGCCCAAGATGGTTTCAATCTCTGACCTC - GTGATCCGCTCACCTTGAGCT	44924
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D	44923	CCCATTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT	44864
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D	44863	TCCTTTCTTTCTTTCTTTCTTT-----CTCT	44833
O	16775	actctcccttatataatttgatgccttltgttcaatcctctgcctgactgctg- gt	16833
D	44832	CTTTCTTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT	44773
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D	44772	TTAGACTTCCCATGGTATGTTTAATAAAAGTTAAAGTAGCAATCCCTTGCTTGTC	44713
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D	44712	AGATCTTAGTGAAAAGCTTTCAAAATTTTCCCTGTTCAATATACATTAGGTGAGTTT	44653
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D	44652	GTCAATATAGGCTTATGTTTGTGAAGTACATTCTTGATACCGATTTGTGTAGAT	44593
O	17010	tctcttaagaaggagtctgaacttaaatctcttcttcgcgcataaagtagt	17069
D	44592	TCTATATCAT - AAGAATATGTTGATATGATCAAAATGCTTTTTCGATCTTAGAGATAT	44534
O	17070	catatggttttgcgccttcaatctgtgtatagatgatacacatatgatttgatat	17129
D	44533	CATATGTTTCTGCTCTTCAATCTGTTCAGCAACGATACACAGTTGATTTGTAT	44474
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D	44473	GTTGATATCATCTTTGATATCCCTAG - ATAGTCTCTACTTACCATGCTGTTATTTT	44415
O	17190	gatttgggttggaattggttctgtcagtaatttgtagaagatttctgcatctgtgcat	17249
D	44414	GATGTGCTGTGCATCAATTTGGTGTAGTATTTGTGTGAGAGATTTTGCATCATAGTCA	44355
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D	44354	CA-----GGGATATTAGTCTGTAGTTTCTTTGTGTGTGTGCTCTCTGTGTTTGGT	44300
O	17310	atcagaagcgataatgacctatagaataagtagtagagaggcgctgcctg---atttt	17366
D	44299	ATCAGGGTATCTGTGCTTGTAGAGTGAAGTGAAGAAATTCCTCCCTGTGAGTTTTT	44240
O	17367	tggaaatagttcagaagatatataactctcttctgatacttgtagaattcggtc	17426
D	44239	TGGAAAAAGTTTGAAGAATTTGATATTTCTTTCTTTGCAAGTTTGGTAGAATTAACA	44180
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D	44179	GTCAACCATTCAGCATATGACTGTGCTATTGGGAGACTTT--TATTAATGATCAA	44123
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D	43942	TCT-----AAATTCAGATTCATTTTCTTAATCTACTAA	43907
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D	43906	GGCTTGCTAATTTTGTATACCTTTTAAAACATACTTTTGTATGTTAACTTT----	43850
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D	43850	--TATATATTATAGTGCATTAATTCATTTATTTGCTAATCTTATATTCTTTTC	43794
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D	43673	CCTATCGTACTACTTTGTGTGTGTGCCATATGTTTGTGATGAGTGTTT - CATTTCA	43615
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D	43614	TTTGTATTATATA--ATATTAACTTCTCTCAAAATTTCTTCACTGACCTTTGGTCA	43558
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D	43557	TTGACGACGATGTTGTAATATGTACGTGATTTGTACATTTTCCAAGTCTCT - TCTTA	43499
O	18136	ttagttcagtttcaattctgtctgtctcgtgaaggcaactgtagatctcagttta	18195
D	43498	TTGATATCTAATTTATTTTCATTTGTGTGTCAGAAAAGATCTTGATATCTTGATTTTA	43439
O	18196	aaaaatttgtgagacttgttltgtgccttaacataigtctgtcttggaagaagtcc	18255
D	43438	AAAAATATTGTGGC - TTGCTGTGGGCTTAACATAGTGTCTATCCGGAAGATGTCC	43380
O	18256	atagcctgaatgaabatgtatattctgcagctgtgtggaagaagcttctgtaagtc	18315
D	43379	ATATGCTAATTAGAA--TGTTATTTGTCATCTATTTGATTAATGTTCTGTAATGTC	43323
O	18316	tgttaagtcatctgtgcctaaagctcagtttagtgcagtggttcttgcgtactcttg	18375
D	43322	CATTTGGTCCATTTGGTCT	

Fri Mar 3 12:08:41 2000

us-09-339-352-9.rge

Page 52

Qy 18553 attataaacgacttccttagtcctttttttttaactgttttllagatggtttt 18612  
| | | | | | | | | | | | | | | | | | |  
Db 43083 AATACATAATGGCTTCTTTGCCCTTTTTTTTTTGCAATCTACTTAAGTCAT 43024

QY	18613	tct	18615
Db	43023	TTT	43021

Search completed: March 2, 2000, 21:20:13  
Job time: 295484 sec

2

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2000, 04:59:16 ; Search time 8603.19 seconds

(without alignments)  
-6776.743 Million cell updates/sec

Title: US-09-339-352-10\_COPY\_15000\_34200

Perfect score: 19201

Sequence: 1 agcacatcctcctcctcctc.....taccaccttagtccacga 19201

Scoring table: IDENTITY\_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl:\*

Word size: 0

Number of hits that pass the threshold: 1642386

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_om:\*  
4: gb\_ov:\*  
5: gb\_pal:\*  
6: gb\_ph:\*  
7: gb\_pl1:\*  
8: gb\_pl2:\*  
9: gb\_pl3:\*  
10: gb\_pr2:\*  
11: gb\_pr3:\*  
12: gb\_ro:\*  
13: gb\_sts:\*  
14: gb\_sy:\*  
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16: gb\_vl:\*  
17: em\_fun:\*  
18: em\_hum1:\*  
19: em\_hum2:\*  
20: em\_in:\*  
21: em\_om:\*  
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25: em\_ph:\*  
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27: em\_ro:\*  
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29: em\_sy:\*  
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36: gb\_hc5:\*  
37: gb\_hc6:\*  
38: gb\_hc7:\*  
39: gb\_hc8:\*  
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41: gb\_hc10:\*  
42: gb\_hc11:\*  
43: gb\_hc12:\*  
44: gb\_hc13:\*  
45: gb\_hc14:\*  
46: gb\_hc15:\*  
47: gb\_hc16:\*  
48: gb\_hc17:\*  
49: gb\_hc18:\*

50: gb\_pl3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19201	100.0	128230	11	HS313L4	299943 Human DNA s
2	950.4	4.9	115218	10	HS159A1	AL034397 Human DNA
3	883.6	4.6	166182	33	CNS01DU	AL133241 Homo sapi
4	868.6	4.5	153781	33	HS01689C5	AL118803 Homo sapi
5	846.2	4.4	30110	11	HS124H12	249918 Human DNA s
6	836.6	4.4	153661	11	HS399M14	296074 Human DNA s
7	830.8	4.3	154269	41	AC011350	AC011350 Homo sapi
8	824.8	4.3	134187	40	AC004704	AC004704 Homo sapi
9	821.6	4.3	99036	40	AC005773	AC005773 Homo sapi
10	804	4.2	96558	11	HS598A24	AL031115 Human DNA
11	804	4.2	61187	11	HS8316	299130 Human DNA s
12	797.4	4.2	104594	11	HS0390L14	AL049550 Human DNA
13	751.6	3.9	111924	11	HS296K21	283821 Human DNA s
14	751.6	3.9	114173	11	HS884M20	AL020591 Homo sapi
15	731	3.8	143376	42	AC012272	AC012272 Homo sapi
16	709.8	3.7	167899	44	AC012027	AC012027 Homo sapi
17	707.6	3.7	84464	11	HS782D21	AL022399 Human DNA
18	701.4	3.7	155960	11	HS288M22	AL035467 Human DNA
19	700.6	3.6	151895	42	AC010142	AC010142 Homo sapi
20	695.4	3.6	93481	40	AF201337	AF201337 Homo sapi
21	691.2	3.6	195960	44	AC013569	AC013569 Homo sapi
22	690	3.6	153428	44	AC015459	AC015459 Homo sapi
23	687.8	3.6	209613	40	AC005539	AC005539 Homo sapi
24	679.2	3.5	130252	44	AC015631	AC015631 Homo sapi
25	674.4	3.5	139515	11	HS38C16	AL035604 Human DNA
26	673.4	3.5	161580	40	HUAC002307	AC002307 Homo sapi
27	673	3.5	39706	11	AC000073	AC000073 Homo sapi
28	672.6	3.5	219580	32	HS855H15	AL078590 Homo sapi
29	672.2	3.5	36955	10	AP000543	AP000543 Homo sapi
30	669	3.5	38993	10	AP000544	AP000544 Homo sapi
31	667.4	3.5	169424	42	AC011961	AC011961 Homo sapi
32	664.2	3.5	100152	40	AC000085	AC000085 Homo sapi
33	662.6	3.5	162473	42	AC012009	AC012009 Homo sapi
34	662.6	3.5	186834	42	AC012082	AC012082 Homo sapi
35	660.2	3.4	178361	40	AC006042	AC006042 Homo sapi
36	656.4	3.4	111648	10	HS16C2	AL049911 Homo sapi
37	654.2	3.4	161973	10	HUAC002038	AC002038 Homo sapi
38	650.6	3.4	326663	40	AF011889	AF011889 Human Xq2
39	649.6	3.4	171801	41	AC009808	AC009808 Homo sapi
40	649.6	3.4	124645	11	HUAC004638	AC004638 Homo sapi
41	644.8	3.4	153060	33	AC007780	AC007780 Homo sapi
42	642.6	3.3	136222	33	AC006477	AC006477 Homo sapi
43	641	3.3	171831	44	AC016706	AC016706 Homo sapi
44	640	3.3	210680	44	AC013530	AC013530 Homo sapi
45	635.8	3.3	135886	10	HSX1S72	U80460 Human Xq13

#### ALIGNMENTS

RESULT 1  
LOCUS HS313L4  
DEFINITION Human DNA sequence from PAC 313L4 on chromosome 1q24. Contains  
ACCESSION Z99943  
VERSION Z99943.1 GI:2887308  
KEYWORDS 1q24.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 128230)  
AUTHORS Pearce,A.  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-1997) Chromosome 1 Project Group  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk  
humquerry@sanger.ac.uk  
On Feb 14, 1998 this sequence version replaced g1:2578084.  
IMPORTANT: This sequence is the entire insert of clone 313L4.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variations annotated may not be found in the sequence submission  
corresponding to the overlapping clone as we submit sequences with  
only a small overlap as described above.  
This sequence was generated from part of bacterial clone contigs of  
human chromosome 1, constructed by the Sanger Centre chromosome 1  
mapping group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1/  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu) where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The true left end of clone 313L4 is at 1 in this sequence. The true  
left end of clone 295C6 is at 122337.  
The true right end of clone 313L4 is at 128230.  
313L4 is from the library RPCI1 constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong.  
For further details see http://bacpac.med.buffalo.edu/  
Location/Qualifiers  
1. 128230  
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277. .384  
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1600. .1760  
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1781. .2080  
/note="AluSg repeat: matches 300. .2 of consensus"  
2081. .2210  
/note="AluSg repeat: matches 136. .3 of consensus;  
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2652. .2780  
/note="MIR2 repeat: matches 44. .139 of consensus"  
3140. .3212  
/note="MIR2 repeat: matches 146. .66 of consensus"  
4164. .4333  
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4334. .4625  
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4630. .4669  
/note="20 copies of 2 mer 88 & conserved"  
4672. .4804  
/note="AluSq repeat: matches 133. .1 of consensus;  
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5281. .5588  
/note="AluX repeat: matches 1. .302 of consensus"  
6070. .6291  
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6575. .6865  
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7450. .7732  
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7732. .8034  
repeat\_region

repeat\_region  
/note="AluY repeat: matches 301. .1 of consensus"  
8082. .8166  
/note="FLAM\_C repeat: matches 49. .133 of consensus"  
8605. .8710  
/note="AluO repeat: matches 190. .302 of consensus;  
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8735. .8909  
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8914. .9169  
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9271. .9759  
/note="MUT2\_internal repeat: matches 1795. .1306 of  
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9760. .10052  
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10053. .10213  
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10272. .10571  
/note="AluY repeat: matches 1. .300 of consensus"  
10573. .11108  
/note="MUT2\_internal repeat: matches 1264. .725 of  
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11111. .11754  
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11751. .11789  
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11876. .12153  
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14223. .14520  
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14796. .15232  
/note="MST4 repeat: matches 1. .426 of consensus"  
15237. .15539  
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15550. .15629  
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15666. .15723  
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17316. .17618  
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17628. .17921  
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18048. .18339  
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18346. .18599  
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18849. .19511  
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19512. .19802  
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19803. .20374  
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20381. .20513  
/note="MIR repeat: matches 225. .82 of consensus"  
20699. .21000  
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23516. .23790  
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24031. .24436  
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24433. .24828  
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24699. .25097  
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25146. .25252  
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26389. .26467  
/note="MER42c repeat: matches 1537. .1457 of consensus"  
repeat\_region

[illegible]

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QY	421	ggtagagacagggtttccaccacgtttagttcaacctgtctctgagctccctaccctcagttta	480
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QY	481	tcctgcctgccttagcctaccacaagctgctggatattaggtgtgaaacacatgaccccaagc	540
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QY	601	atatacacacatatataattatgtttatcttcttccttgagctgcctgcctgcagatgaa	660
Db	15600	atattatcacacatatataattatgtttatcttcttccttgagctgcctgcctgcagatgaa	15659
QY	661	tcctctgcacaggccacagaaaagtgcacctggagacatgaaatcgaagtgctgttgttaat	720
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QY	721	gaattattatgggtggtgcagagtgcttaccagctcttggtttggtttaattgaagtt	780
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QY	781	ttaagtagaagagccttttgaattcttgaaagaataatlaaagcttccaaaatctcaagat	840
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QY	841	gtaatttaccctatacagaatgtaaaatgagctctcaagttctctgtatgtctgcctt	900
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QY	901	cccatataacatataacatctgcatacaccagagaagccccaaggagcctgtgaagag	960
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QY	961	ccatataccctggggaataatagctagaagaactttgtctctccctaccctccaaagctg	1020
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QY	1201	cagttctcggagctcatcaagctcttcccatccctccctcctgtcttgttttgtatcgtttac	1260
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QY	1261	ttcctcgtgcctctccctctcccgctccacaactgtgagctccatagttcatgttataatcat	1320
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Db	18660	TATAACAAGTATAAAGATGATACCGCTTAACATAATATATATGGGAGATACCTTAAATGATAC	18719
OY	3721	ttccaataaaagaatacttcgcaactttaaaataacatacatagatgcctgaag	3780
Db	18720	TTTCAATAATAAAGATACCTTCCCAACTTTAAATAAATATATATGAGTCCGAGAGG	18779
OY	3781	aattccttaaggagatcacaagtcatacagtcataccaataacagaaataggaaactaag	3840
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OY	3841	tttatcttgaaatggatgttgaaagaatttcctcaactcgtggagtgttcgtttactcgt	3900
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OY	3901	ctgaactgttcctctttgcacacacaaaagctccttaagtttaagtcccaagctattactctg	3960
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OY	3961	ttttcgttgcaattgctcttgggtccttggtcaatgaagcttcgtctaagctaatgtcag	4020
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OY	4021	aagggttttccaaegttctctccacagaaattttaagttcaagctctagaattcaagtc	4080
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OY	4141	cctaaatgtyggttaagccaattatccacagacaaagtgttgaataaggygtccttcccca	4200
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OY	4201	cttgatgttttctgttctgttcttgcaatgaatcagatagctgaatgatgttgattatctt	4260
Db	19200	CTTGATGTTTTTGTGTGCTTGTCTCAATATATCATGATGAGCGTAAAGTATTTGGTTATTTT	19259
OY	4261	tgggtctctcatattgcttccttggtcctatgctatgctcattttatcaagtlaccagagctgc	4320
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Db	19380	TATGACAGGCTCTTTTGGTTCATATGAAATTTTAGGATGTGTTTTTCTAGATCTGTGAA	19439
OY	4441	aactgatggtgattatttgatagtggaattgctgtgaattgttgattactcttgggaagat	4500
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OY	4561	tgcgaatgagtgatcttgccctgaactgcacaactcctcctcctctgtgttcaagcaattcctct	4620
Db	19560	TGCATATGGCGTATATTGTGCTATACGTCAACCACTCTCGCTCTGTGGTTCAAGCAATTCCTCT	19619
OY	4621	gacctaacctcccaagtagctggaactcgaagcgacatcaatcaagcccaagtaattttgtga	4680
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OY	4681	tttttaagtagaagcggggttttacaatgcttaagcaagctgtgtctcgatcctcttgacctcg	4740
Db	19680	TTTTTAAGTAGAACGGGTTTTACCATATGTATACCAAGCGTGGTCTGTGATCTTTGACCTCG	19739

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Oy	5881	ctgagcgaggaagaacacttgaaaccggyggtcagaaglttcagtgaacgagatcgcac	5940
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Oy	5941	cacttcactccagccttggcggaagagcgaaactcaagttcgaaaaaaanaaaaaaaga	6000
Db	20940	CAC TTCAC TCCAGCCTGGCGGCAAAAGCAAACTCAGTCTCAAAAAAANAANAAGA	20999
Oy	6001	acc tccaaatagcaglttgccactttctctctccaagltccacataagacctataa	6060
Db	21000	ACCTCCAAATAGCATTGGCCATTGTCCTCTCCAAAGTTCATATATACCTTATATA	21059
Oy	6061	agtttagactccaacactagtaaatlttttccacttgtttcgttaattatctc	6120
Db	21060	AGTTATAGCTCCAACTATATATATTTTTTCCACTTCTTGCTGTAATTTATTTTC	21119
Oy	6121	cattaatgggagtaagatacgaacagataatgttactgtlcatcaglttaagaata	6180
Db	21120	CATTAATTTGGGAGTAAGATCAAAAACAGATATGTTTACTGTCAATTAAGATTA	21179
Oy	6181	atgttgctcttaectccgcagagcggaatgatacactacttctccccaactgcgaat	6240
Db	21180	ANGTGTGCTTACTCCGAGAGCGGATGGAATCACTACTTCTCCCCACATGCAAAAT	21239
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Db	21240	TGGTTAAGTGTGGAAACTGATGATACCTATATGTGCACCAAGACGTACGAAAGGTTT	21299
Oy	6301	atgactcacttactagagccttttggggagcagagcgagcttcccatgcagtacaag	6360
Db	21300	ATGACTCACTTACTAGGCGCTTTTGGGGAGACAGGCGCTTCCATGCGAGTACAAG	21359
Oy	6361	aatgcttgagagaacaggaagaagatactgctctcctttatggtataagttgtcga	6420
Db	21360	AATGGCTTGAGAAACAGAAAAAGGATATGTGCTCTCTTTATGTGTAAAGTTGCTGA	21419
Oy	6421	gctcagtgagtagagtcctctataatgcgccctcgaacgagtcgtgttgaactccact	6480
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Db	21480	GTTCCAAAGGATGCGTCACTTGGCGTTTCTTATGCTTGCCCTGAGGAAAGGGGTACAG	21539
Oy	6541	cttgaagaactcttgcgcatacaaatcaaaaaatgtgtcagaagcctttctcaaatata	6600
Db	21540	CTTGAAAGCTCTGGCAGTCAAAATTCAAAAATGATGTACAGCTCTTTTTCAAATATA	21599
Oy	6601	ttttaagltgcttgcattgtttatgttataatgggcaaaatcttgcattgtactaacac	6660
Db	21600	TTTTTAAGTGCTTGATCATGTGTTATGTTATGGGCAAAATCTTGCAATGTCTTAACAC	21659
Oy	6661	catgctactaatagtgtaataagaattcacagacactaatgttcaagaatgttttgaa	6720
Db	21660	CATGTCACCTAATAGTGTGAATGAAGATTACACAACTAATGTCAAGATGTTTTGGA	21719
Oy	6721	ccttgaacaagaagataatcctgtgtgtcttctttaaacaacgaaataactaacatcc	6780
Db	21720	CCTTGAACACAGGGAATATCCGTGTGCTTTTAAAAACACGGAATAATCTTAACATGC	21779
Oy	6781	tatttcttggtgttaacacatgatagcctgaatgttgggtatgttgcctgggtcac	6840
Db	21780	TATTTTGTGTTGGTTAACACTGATATGTGAAAGTTGGGATTAATGATTCCTGGGTAC	21839
Oy	6841	tatgggcaagaagacttttttggtttcttgaattatagttatagattactagcttctgt	6900
Db	21840	TATGGCAAAGAGCTTTTTTTTGTGTTTGTATAGTTTATGATATTACGATTTTCTGTGT	21899
Oy	6901	ttgttcacattcttttcttatttataaacaagtlttbaataaatgggcactctattt	6960

Dp	21900	TTTGCAATATCTTTTGGATTTTATTTATTAACATGTTTATTAATAAATGGCACTCTATT	21959
Oy	6961	tcaaaccttaataataagaccctattctactatgcatcccggtgtttaatctcgaact	7020
Dp	21960	TCAAACTTAATAATAAGACCTCAATTTTCTATGCAATCCCTGGGTTTAATTTCTGAGCT	22019
Oy	7021	aagaacaagaagatatgaagaaccaaattcggtaaatccagagctctagatgccaagaag	7080
Dp	22020	AAGAACAAGAAGATAGAAAGAACCAAAATTTGGTAAATTCAGAGCTTAGAGCCAGAAG	22079
Oy	7141	acaacatgcctctcaggtgttggtttctcgccttcctctaaattctctgacaggttttaa	7200
Dp	22140	ACAAATGCTTTCCAGGTTTGTTGGTTTACTGCTTTCAATTAAATTCTGCACAGTTTAA	22199
Oy	7201	tatttaatatctcgtatatttggatatgctatgccttaacaattgttgcgagtcatagcaca	7260
Dp	22200	TATTTTAAATCTCTGATATTGGATGGATAGCCCTTAACAATGTGGCGAATCATAGCCACA	22259
Oy	7261	ttttattctcttggggaaacccggaataatgtgtcttcctccagtggtgttcaatta	7320
Dp	22260	TTTTTATTTCTGGGACACAGAAAATATGATGTCTTACCCTCACTGGATGTCTTAATTA	22319
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Dp	22320	CATGAACATATGACATTTTTCACCTTTTAAGCTCTTTAAATTAATAAATTCATTTATA	22379
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Dp	22380	CTTCAGAAAAAATACCTTATGATTTAAACACACGATTTGGGGAGACTTTCAGATGGATATG	22439
Oy	7441	ccttgagtttcctcttgaaggaaagatggagatgttggcccaacggaggttggtttgtgagga	7500
Dp	22440	CCTTGAATTTGCTTTGAAGGAGAGAGATGGGAGTTGGCCCAACGGAGTGGGTTGGTGAGA	22499
Oy	7501	aggcatctcagaactggaagataagcatatacaagcatatlaaagaagtgtcgtgtgttggg	7560
Dp	22500	AGGCATCAGACTGAGATGAGATAGCATATACAGATATATTAAGAGTGTGCTGTGTGGGG	22559
Oy	7561	aaagggctcagaagcttctgattgtggcaaaaatgtaggctcttggagatagaatagaataa	7620
Dp	22560	AAAGGGCTTAGAAGTTTGATGTGGCAAAAATGTAAGCTCTGGGATAGATAGAAATGATTA	22619
Oy	7621	actggtctgaatgtgaacctggaagcagaaccttgaagaagctctgtgtgcgtgcgaagga	7680
Dp	22620	ACTGCTCTGAATGCTAAGCTTGAGCGCAACCTTTGAAAGGCTCTGTGTCCTGTCGACAGGA	22679
Oy	7681	gttgaggtctcttggcaatgttaaggcagcaattgtaagcagctctccctccctgttgca	7740
Dp	22680	GTTGAGCTGTCTTGGCATGTTAGGCAACCATGTGTAAACAGCTCTCCCTCCTGTTTCA	22739
Oy	7741	tcagaaaggggttgggcagcatttggcaccaataaagaagaagtgtaagaacaatacgaagt	7800
Dp	22740	TCAGCAAAAGGGGTGGCGACCATTTGCACCAATTAACGAAGAGTGAACAAATPACTAATGT	22799
Oy	7801	cgaataagaactctcagcacaagagttctcccaaatgtaaaagggtctgacaccttggaaatcga	7860
Dp	22800	CGAATAAGATCTCTAGCACAGAGTCTTCCAAATGGAAGGGCTGCACCTCGGATTCAGA	22859
Oy	7861	tggaaaggaagaacttaccaaagggtgtctatttccctctgctcgtgtgtgaatgaat	7920
Dp	22860	TGGAAGGGAAGAACTTTACCAGGGGGTCTATTTCTCTCTCCTCTGTTGTGATAGAAAT	22919
Oy	7921	ggggtctcagttgcccgttttgaagaccgtttgttggcgaagctgtgtgtaacaagtctgt	7980
Dp	22920	GGGCTTCACTGCTGCTTTTGAAGACCTGTTTGTGTGGCAACTGTGTACAAAGTTGTATG	22979
Oy	7981	aaaaatgaggaatgcttctcagaggcagatlaatccatttgaatggaatlttagagct	8040
Dp	22980	AAAAATGAGGATGCTTTCAGAGGCGATATTAATCATTTGGATGTGAATAATTGGAGGT	23039

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D	25320	CTTTCACAAAATATACAAATTTCACTCATCTTCCAGATTTGGTGTTCACGACACTCATGCT	25379
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QY	12541	gaagacagaaaggaataatacatatttagtaagagtcaccatcaaaatggtgtgaattt	12600
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QY	12601	aaaaaataactcttaaggaaccltgagtgatgtcattttgacagataaatacgtagaatta	12660
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QY	12661	cttactatcaagaataataatgtatgcgcggcgcggttgccacgctcgtatcccaagc	12720
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QY	12721	actttggagagcctlgagtgggcggaatcacttggagtcagagagtcgagaacatccctggcc	12780
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QY	13501	gagataaaatcaagltgcaatctttcaataaatctccctgaccccttcaatcttccaatt	13560
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QY	13561	ttgacttaatatagctacataagctctatttgcacttcaagggaggttgtagtagaa	13620
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QY	13921	tccattccccctccatatttactcttcgttcaagggtagaggttcaacttgaacct	13980
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QY	13981	ttctcgcaagtgaatgaatcagltgcgtatataatcaatcaactctttgcagaaattttcaaga	14040
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QY	14281	aggagtgtgtagtctcaacaggggagctgaagttaattgcaaggggagattgtgctttcac	14340
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QY	14341	tgaagagtgctgtccgtcgtagagctacagccatagagtgctgtgagaaattactgaagagtg	14400
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QY	14461	tcttgaaattctgtaagcttccagaggtgtggccttggtccaaagctgtgtgtagtatagcc	14520
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QY	14521	tgaagtagactgtgcgtggtggcatttgaaggaatgtagagcaaatctaatccagctgcg	14580
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QY	18121	acagcccttgcctctcttgggggtgcagacagccgltcaattaaigtgggtgtgtagggga	18180
Db	33120	ACAGCCCTTTGCCCTCTTGGGGGTGCAGACACCCTGATTTAAATGGGGGTGTAGGAGGA	33179
QY	18181	gcatttacaaggaaggaagacagaatgtcggggagacacagggttgaggaggtgtgggacag	18240
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RESULT 2  
HS159A1/c  
LOCUS  
DEFINITION Human DNA sequence from clone 159A1 on chromosome Xq12-13.3.  
ACCESSION AL034397  
VERSION AT034397.1 GI:3980338  
KEYWORDS HTG; ca repeat polymorphism; DXS1213; Glycoprotein P43;  
SOURCE Heterogenous Nuclear Ribonucleoprotein G; HNRNP G.  
ORGANISM human.  
REFERENCE 1 (bases 1 to 115218)  
AUTHORS Pearce, A.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
COMMENT During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence is the entire insert of clone 159A1. This sequence  
has been finished according to sequence map criteria as follows. An  
attempt is made to resolve all sequencing problems, such as  
compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key  
This sequence was generated from part of bacterial clone contigs of  
human chromosome X, constructed by the Sanger Centre Chromosome X  
Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/ChrX  
159A1 is from the library RPc16 constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong. For further  
details see http://bacpac.med.buffalo.edu/ VECTOR: pPAC4.  
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2840. .2940  
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3146. .3301  
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4047. .4162  
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4439. .4563  
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4827. .5188  
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5386. .5557  
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5728. .5982  
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6334. .6493  
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6727. .6932  
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7748. .8631  
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9161. .9251  
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9310. .9415  
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9699. .9781  
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9816. .9892  
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10335. .10608  
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11066. .11103  
/note="match: STR 224013; genomic marker DXS1213"  
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complement(11067. .11102)  
/note="18 copies of ca 100% conserved; differs from  
224013"  
11546. .11658  
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11961. .12094  
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12196. .12267  
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12368. .12482  
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12706. .12777  
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AA972857 AA436814 R62969 W74268 H05057 N78991 AA813538  
AA939378 AA627735 AI168499 R39812 R59156 R56602 D79546"  
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/product="dA159A1.1 (novel protein)"  
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join(14224. .14278, 20392. .20748, 21473. .21754, 26110. .26172,  
26696. .26773, 29093. .29197, 31360. .31381, 31722. .31959)  
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Db 100940 TAGGTCATTGACACACATTGATTTTACCATTATGACACAGCATGGTGT-CA 100882
QY 4854 gttatgcatcgtgtagcttcttcacgaagtgtctgtagttcttctctagaagtg 4913
Db 100881 CTTGGGTGATCATATATTTCTTTACAGCAGTGTGTTGATGTTTCTTTGTA 100822
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QY 4974 gaaggagttgagttctgtagttctcagctgtgtgtgtgtgtgtatagaaggt 5033
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QY 5034 actgattgttcaatcaattctgcacatcgaa--ctgctgaattcttctcagtt 5091
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QY 5092 gggagctcttgagagagctcttagagttctcaggttaaacagctctatcacga 5151
Db 100646 AGAGACTTTTGGAAAAGTCTTAGGCTTTCTTAGGTAATATCATATCATCA 100587
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QY 5272 tgcctctcagttctcagaaggaactctcaacttccctcatctatattgtg 5331
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QY 5332 gctgtgagttgtcatagatgctttatcatattgagatgagt 5375
Db 100406 GCTTTGTTGTCATGATGACTTTAGTGCATTTAGATGATGT 100363

RESULT 3
CONSOLID 3
LOCUS 3
DEFINITION 166182 bp DNA HTG 27-NOV-1999
PROGRESS *** in ordered pieces.
ACCESSION AL133241
VERSION AL133241.1 GI:6478098
KEYWORDS HTG; HTGS.PHASE2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166182)
REFERENCE 1
AUTHORS Direct Submission
TITLE Submitted (26-NOV-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage, etc.
Contig order : 10 6 3 4 8 9 7, 1000 N's separate segments Contig 10
: length 72699 bp
Contig 6 : length 11379 bp
Contig 3 : length 1715 bp
Contig 4 : length 1913 bp
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Contig 8 : length 12095 bp
Contig 9 : length 54546 bp
Contig 7 : length 7987 bp.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
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/db_xref="taxon:9606"
/chromosome="14"
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using the e-PCR software (G. Schuler)"

BASE COUNT 48652 a 28853 c 29318 g 53357 t 6002 others
ORIGIN

Query Match 4.6%; Score 883.6; DB 33; Length 166182;
Best Local Similarity 79.4%; Pred. No. 3.9e-150;
Matches 1285; Conservative 0; Mismatches 204; Indels 129; Gaps 15;

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Db 48092 CCTTTGCCATGCAAAAGCTCTTTA-----CCAGCTATGATCTTTGCTTTAT 48142
QY 3970 cattgtcttgggtctgtgtcagaagctgtgc9laagcctaigtctagaaggttt 4029
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QY 4150 ggttaagcaattatcccaagcagctgttgaatgaagtggtctctcccaactgatt 4209
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QY 4330 tttgacctataagtagtttgaatcaagtaagtgtatgtctccagatt----- 4380
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QY 4422 ttttctcgtctctggaacatgagtgtgattttg-atgggaattcgtgtgaattg 4480
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QY 4325 atgacgtgagccttatagtgtgttgaatcaggtaatgtatgtatgcctcaagatt----- 4380
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QY 4380 -----gtatcaggctctcttcttcttcttctcattatgaatttagg 4417
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QY 4418 atcgcttttctagctctgtgaaactgacgtgtatctttagtgggaattcgctgaat 4477
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QY 5223 taggaactccaactttgtgaagagagtgtaagatgaggcatcttctcattcc 5282
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RESULT 5
LOCUS HSL124H12 30110 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from cosmid L124h12, Huntington's Disease
ACCESSION Z49918.1 GI:887461
VERSION 4p16.3.
KEYWORDS 4p16.3.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 30110)
AUTHORS Dodsworth,S.
TITLE Direct SubMISSION
JOURNAL Submitted (26-JUN-1995) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RO, England. E-mail: goss@sanger.ac.uk
COMMENT IMPORTANT: This sequence is not the entire insert of clone
L124h12. It may be shorter because we only sequence overlapping
sections once, or longer because we arrange for a small overlap
between neighbouring submissions.
The true left end of clone L124h12 is at 1 in this sequence. The
true right end of clone HM2 is at 18185.
The true left end of clone L108f12 is at 30011.
The start of this sequence (1..100) overlaps with the end of
sequence Z49250 ( HM2 ).
The end of this sequence (30011..30110) overlaps with the start of
sequence Z49235 ( L108f12 ).
L124h12 is from cosmid library LA04NC01 constructed at the Human
Genome Center, Los Alamos National Laboratory, NM 87545 under the
auspices of the U.S. Department of Energy. The library was
constructed using flow-sorted human chromosome 4 from a
Hamster-Human hybrid cell line ( UV20HL21-27 ) containing human
chromosomes 4, 8 and 21.
VECTOR: sCos1
L124h12 is contained in a clone contig spanning
2Mb which is described in Baxendale et al, Nature Genetics 4 ( 1993
) 181-186. See also Myers et al, Cytogenet Cell Genet. 66 ( 1994
) 218-230.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="LA04NC01"
/clone_line="UV20HL21-27"
/clone="LA04NC01-124h12"
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/note="Alu repeat: matches 308. .1 of consensus"
1440..1716
/note="Alu repeat: matches 1..308 of consensus"
2368..2451
/partial
/note="Alu repeat: matches 59. .150 of consensus"
2609..2779
/note="MTIE element fragment"
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repeat_region 5115.5406 /note="MER7 element fragment"  
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repeat_region 5501.5548 /note="MER29 element fragment"  
repeat_region 5673.5890 /note="MER17 element fragment"  
repeat_region 6124.6496 /note="MER29 element fragment"  
repeat_region 6503.6835 /note="MER17 element fragment"  
repeat_region 7568.7747 /note="MER18 element fragment"  
repeat_region 7754.7802 /note="Alu repeat: matches 277. .69 of consensus"  
repeat_region 7977.8201 /note="Alu repeat: matches 48. .1 of consensus"  
repeat_region 8202.8491 /note="MER4A2 element fragment"  
repeat_region 8495.8753 /note="Alu repeat: matches 1. .308 of consensus"  
repeat_region 8768.8930 /note="MER4A2 element fragment"  
repeat_region 11621.11925 /note="Alu repeat: matches 129. .308 of consensus"  
repeat_region 11929.12012 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 12013.12054 /note="Alu repeat: matches 142. .60 of consensus"  
repeat_region 15142.15215 /note="Alu repeat: matches 205. .164 of consensus"  
repeat_region 15540.15632 /note="37 copies of 2mer 81 & conserved"  
repeat_region 15842.16121 /note="LI element fragment"  
repeat_region 17390.17691 /note="Alu repeat: matches 296. .1 of consensus"  
repeat_region 18254.18336 /note="Alu repeat: matches 1. .308 of consensus"  
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repeat_region 18818.19106 /note="Alu repeat: matches 226. .1 of consensus"  
repeat_region 19149.19434 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 19483.19775 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 20111.20402 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 20584.20872 /note="Alu repeat: matches 1. .308 of consensus"  
repeat_region 21074.21363 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 22237.22573 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 22720.24165 /note="LI element fragment"  
repeat_region 24188.24479 /note="LI element fragment"  
repeat_region 24480.25929 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 25954.26244 /note="LI element fragment"  
repeat_region 26273.26374 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 26484.26773 /note="LI element fragment"  
repeat_region 26777.27337 /note="Alu repeat: matches 308. .1 of consensus"  
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repeat_region 27628.27913 /note="Alu repeat: matches 308. .16 of consensus"  
repeat_region 28030.28740 /note="LI element fragment"
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GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2000, 10:38:02 : Search time 12284.3 Seconds  
(without alignments)  
6147.117 Million cell updates/sec

Title: US-09-339-352-7\_COPY\_1\_20000  
Perfect score: 20000  
Sequence: 1 gatcattcgttctcaggcc.....gaacttaggtctcttgya 20000

Scoring table: IDENTITY\_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:\*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
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10: em\_est10:\*  
11: em\_est11:\*  
12: em\_est12:\*  
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75: em\_est31:\*  
76: em\_est32:\*  
77: em\_est33:\*  
78: em\_est34:\*  
79: gb\_gss1:\*  
80: gb\_gss2:\*  
81: gb\_gss3:\*  
82: gb\_gss4:\*  
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84: em\_gss2:\*  
85: em\_gss3:\*  
86: em\_gss4:\*  
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91: gb\_gss9:\*  
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93: em\_gss6:\*  
94: em\_gss7:\*  
95: em\_gss8:\*  
96: em\_gss9:\*  
97: em\_gss10:\*  
98: em\_gss11:\*  
99: gb\_gss10:\*  
100: gb\_gss11:\*  
101: em\_gss12:\*  
102: gb\_gss12:\*  
103: gb\_gss13:\*  
104: gb\_gss14:\*  
105: gb\_gss15:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472.4	2.4	493	B36003	B36003 HS-1031-A2-
2	443.8	2.2	842	A0897632	A0897632 HS-3135_A
3	420.4	2.1	590	A0706541	A0706541 HS-5534_B
4	410.8	2.1	501	A1950087	A1950087 wq05c02.X
5	405.6	2.0	524	AL049113	AL049113 DKFZp434D
6	391.8	2.0	457	N70208	N70208 za55e09.s1
7	391.2	2.0	646	AG545781	AG545781 CITR-FI-



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C 8 389 1.9 405 90 B99738 C1T-HSP-228
9 386.8 1.9 422 30 AA251874
10 380.8 1.9 473 31 AA283144
C 11 373.8 1.9 538 100 AO277241
C 12 371.2 1.9 579 100 AO316362
C 13 357 1.8 2971 80 AF101960
C 14 355.8 1.8 866 87 AO752136
C 15 324.4 1.6 2971 80 AF101960
C 16 322.8 1.6 666 24 N36809
C 17 319.4 1.6 695 43 A1174916
C 18 313.8 1.6 599 90 AO058824
C 19 308.4 1.5 334 34 AA488964
C 20 306.6 1.5 547 82 AO694304
C 21 296.4 1.5 559 61 A1819225
C 22 288.2 1.4 582 102 AO417202
C 23 287.2 1.4 500 61 A1821380
C 24 285.4 1.4 688 81 B69266
C 25 284.4 1.4 731 103 AO474778
C 26 283.6 1.4 727 103 AO484818
C 27 283 1.4 428 91 AO129730
C 28 282.8 1.4 689 79 AO019547
C 29 282.4 1.4 702 102 AO395067
C 30 282.2 1.4 520 81 B60352
C 31 282 1.4 469 82 AO692948
C 32 282 1.4 555 105 AO629757
C 33 281.6 1.4 490 81 B39755
C 34 280.4 1.4 812 81 B05781
C 35 279.6 1.4 732 90 B94490
C 36 279.4 1.4 730 89 AO898190
C 37 279.2 1.4 516 90 AO003835
C 38 278.4 1.4 737 91 AO116454
C 39 278.2 1.4 463 42 A1089421
C 40 277.8 1.4 306 25 N46026
C 41 277.8 1.4 621 100 AO269192
C 42 276.8 1.4 403 35 AA594479
C 43 276.6 1.4 509 102 AO381842
C 44 275.6 1.4 474 81 B39296
C 45 275.2 1.4 827 82 AO741201
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## ALIGNMENTS

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RESULT 1 B36003 493 bp DNA GSS 17-OCT-1997
LOCUS B36003 HS-1031-A2-H02-MR-ab1 CIT Human Genomic Sperm Library C Homo
DEFINITION sapiens genomic clone Plate-CT 811 Col-4 Row-O, genomic survey
sequence.
```

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ACCESSION B36003
VERSION B36003.1 GI:2535372
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 493)
Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Traioccoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Unpublished (1997)
CONTACT: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT 811 row: O column: 4
Class: BAC ends
High quality sequence stop: 493.
```

## FEATURES

source

Location/Qualifiers

1..493

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="Plate-CT 811 Col-4 Row-O"

/clone\_11b="CIT Human Genomic Sperm Library C"

/sex="M"

/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

## BASE COUNT

119 a 124 c 108 g 141 t 1 others

## ORIGIN

## Query Match

2.4% Score 472.4; DB 81; Length 493;

Best Local Similarity 99.6%; Pred. No. 7.9e-44;

Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## Query

786 atgtgacttcttgagacatttgaccagatgctctctgtttaaggacaaattagaatt 845

## Db

19 atgtgacttcttgagacatttgaccagatgctctctgtttaaggacaaattagaatt 78

## Query

846 ctcaacttgcacaaacacacagtagaactaagctagctccatctctctctctctt 905

## Db

79 ctcaacttgcacaaacacacagtagaactaagctagctccatctctctctctctt 138

## Query

906 gtagatgacttctactctgttgcacacagtagaactaagctagctccatctctct 965

## Db

139 gtagatgacttctactctgttgcacacagtagaactaagctagctccatctctct 198

## Query

966 caactctgcctctctgttgcacacagtagaactaagctagctccatctctctgt 1025

## Db

199 caactctgcctctctgttgcacacagtagaactaagctagctccatctctgt 258

## Query

1026 taaaggac 1085

## Db

259 taaaggac 318

## Query

1086 acatgttgcac 1145

## Db

319 acatgttgcac 378

## Query

1146 cccaaagctggtggttgcacacacacacacacacacacacacacacacacac 1205

## Db

379 cccaaagctggtggttgcacacacacacacacacacacacacacacacacac 438

## Query

1206 acgaacataaataagcactcttttgaagacttgaagccttgaagccttgaagc 1260

## Db

439 acgaacataaataagcactcttttgaagacttgaagccttgaagccttgaagc 493

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RESULT 2 AO897632 842 bp DNA GSS 10-NOV-1999
LOCUS AO897632/C HS_3135-AL_A10-T7C CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate-3135 Col-19 Row-A, genomic survey
sequence.
ACCESSION AO897632
VERSION AO897632.1 GI:6353822
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 842)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,K.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
```



QY	16240	taattaagaataagatcatgctagaagtaggttaggtccttaatccaataaactgtatgcc	16239
Db	407	TAGTTAAGATATAGATCATGCTAGAGTATAGGCTTAAATCCATTAACCTGATGCC	348
QY	16300	ttataaaaaggagaattttgacacacaacaacacagaaggagaatgycatgtgacatgaa	16359
Db	347	TTATATAAAAGGAGAATTTGGACACMACACACACANAGGAGAAATGCCATGTGACATGAA	288
QY	16360	ggcagagaatttaggttgaagctcttcaacagccatcttttgaacacgaagtgtccagcaa	16419
Db	287	GGCAGAGATTTAGGGTGAACGCTTCTTCAAGCCATTCTTTGGACACCAAAAGATGGCCAGCA	228
QY	16420	ccaccagaagcttagcaggttggycatgaaacagatcttcttcatagtgtccagaagaanaa	16479
Db	227	CCACACAGACGTAGACAGGTGGGACATGAAGAAACAGATTCTTCATCATGTGCACAGAGAAA	168
QY	16480	gattccttgatcttaagatcttaacccctggagaaacatatagaanaattctgttgaagcc	16539
Db	167	GATGCTTGATCTCGATCTCCATCCCGTAGACATATGACAAATNTCTGTTGTGAAGC	108
QY	16540	atccatttgttagtactctttttaccagaagcccccggctagtgaaatacagcacttagtattgc	16599
Db	107	ATCATTTTGTGTACTTNTNTACAGAGCCCGCGCTAGTGAATACAGCACTTAGTAGTTC	48
QY	16600	ctgaacataag 16609	
Db	47	NNGAACATAG 38	
RESULT	4		
AI950087			
LOCUS	AI950087	501 bp	mRNA
DEFINITION	w405c02.x1 NCI-CGAP_Ki67 Homo sapiens CDNA clone IMAGE:2470370 3'	EST	06-SEP-1998
ACCESSION	AI950087		
VERSION	AI950087.1	GI:5742397	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 501)		
COMMENT	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index		
COMMENT	Unpublished (1997)		
COMMENT	On Feb 17, 1998 this sequence version replaced gi:2889741.		

**FEATURES**  
**source**

seq primer-40UP from Gibco  
High quality sequence stop: 388.  
Location/Qualifiers  
1. 501  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2470370"  
/clone\_lib="NCI\_CGAP\_Kid12"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH103"  
/note="Organ: Kidney; Vector: pT7T3-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Kids was  
prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1321912-1325831, 1471366-1472933 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "

[illegible]

	RESULT	5
LOCUS	AL049113	
DEFINITION	AL049113 524 bp mRNA	EST 29-SEP-1999
ACCESSION	DKEFZ433BD1519.r1.434 (synonym: htcs3)	Homo sapiens cDNA clone
VERSION	DKEFZ433BD1519.mRNA sequence.	
KEYWORDS	AL049113.1 GI:4728423	
SOURCE	EST.	
ORGANISM	human.	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
TITLE	Eutheria; Primates; Catarrhini; Homnidae; Homo.	
JOURNAL	1 (bases 1 to 524)	
COMMENT	Ottewaelder,B., Obermayer,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.	
	EST (Ottewaelder, et al.)	
	Unpublished (1995)	
	On Jun 5, 1998 this sequence version replaced gi:3189292.	

**MAPS**  
 Am Klopferspitz 18a D-82152 Martinsried, Germany  
 This is the 5' sequence of the clone insert  
 from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ): Email: s.wiemann@dkfz-heidelberg.de;  
 sequenced by MedGenomix within the cDNA sequencing consortium of  
 the German Genome Project.



```
Db 421 GAGTAATAGCATGCAAGCTCTCTC 447
|||||
RESULT 7
LOCUS A0545781 646 bp DNA GSS 28-MAY-1999
DEFINITION CITBI-El-2629B18.TF CITBI-El Homo sapiens genomic clone 2629B18,
genomic survey sequence.
ACCESSION A0545781
VERSION A0545781.1 GI:4905024
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES
Location/Qualifiers
source 1..646
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2629B18"
/clone_1lb="CITBI-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 206 a 126 c 70 g 244 t
ORIGIN
Query Match 2.0%; Score 391.2; DB 104; Length 646;
Best Local Similarity 81.0%; Pred. No. 6,5e-35;
Matches 530; Conservative 0; Mismatches 113; Indels 11; Gaps 6;
QY 18946 ttgtttaagaagaataatttgtaataagtcagaagaatgagacatgccaagaattat 19005
|||||
Db 646 TTGTTAAAGAAAGAAATGTTCCACCAGACAGAAAGTTAAGCATGTCAAG-ATTGT 588
|||||
QY 19006 ctgggaagtcataagaacgatgttataaaaattatgtaaaaaaatgtataatt 19065
|||||
Db 587 CTGTGGAAGTATGAAAATGTTATTAAGAAATTTATGCAAGATGTCATTAATT 528
|||||
QY 19066 gaaagtaaaagcctctg-agtactatgaaagaacagttatgtgcaagtgcataa 19124
|||||
Db 527 AAAAGTAGGCTCTCGTGTGTAAGAACTTTTGAGAAACAGTTTATGTCAGAGTGCTGTA 468
|||||
QY 19125 gaaaagtaaatatacttctgtgtaaaagatgagaagagcatagaagtgtgatttc 19184
|||||
Db 467 GGAAGTAATAATATCTTTGTGTAAGAAATTAAGAGGCAATAAGATGTGATTTT 408
|||||
QY 19185 acctacattaaaggtaaaaaattatgtttgaaagtttaagcaagtttaaatgt 19244
|||||
Db 407 ACCTACATTTAAAGGTTTAA-----ATTGTTTGAAGGTTTAAAGCAAGTTTGAACGT 354
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QY 19245 taattgtataaaaaaatctgtgtgtataaactaattagctaaagataaaagtatcatcc 19304
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```

```
Db 353 TAATTGT-AGAGGAAGTTCTGTGTAAACATATTGGCTAAAGTTAAAGGGATATCATCC 295
|||||
QY 19305 agttttctgtgactggacattaagaatgaataaaatgcacaaggtttcttgaagcccaa 19364
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Db 294 AGTTTCTGTAAACAGGACATTTTAATTAAGACACAAATGGGTTTTTCTTAAAGCACTAA 235
|||||
QY 19365 ccgtgctttaacaaaataataaagaagtttaaaaagagtcgtgaanaaacttaccattg 19424
|||||
Db 234 CTGTGTTTAAACAAAATATATAGAGGTTAAAAAGAGTGTGTAATAATGTTACCTATAG 175
|||||
QY 19425 tcaaacatgaaaaattggataaatatgctcctagaggtttataataaattgaattacat 19484
|||||
Db 174 GTTAGACATTACAAATTGGATAAATATGCTACCAAGATTTTAAATCGAGTTTAACAT 115
|||||
QY 19485 taataacacctaattaaaggttaaaattagcttctgtgtaaaatcatcacaagaa 19544
|||||
Db 114 TAATAGCACACTAATGAAAAGTGAAGTTTGAAGATCTGTAT-AAATCCATACAGGAA 56
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QY 19545 gtattataataataatggttttagctt-cttggtctaaaactataa 19597
|||||
Db 55 GCATTGCGAATATAAATCTGCTTTGGCTTACTTGTGTCAAAAAATATAA 2
|||||
RESULT 8
LOCUS B99738 405 bp DNA GSS 26-JUN-1998
DEFINITION CIT-HSP-2284G20.TF CIT-HSP Homo sapiens genomic clone 2284G20,
genomic survey sequence.
ACCESSION B99738
VERSION B99738.1 GI:3026289
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
FEATURES
Location/Qualifiers
source 1..405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="GDB:7148351"
/clone="2284G20"
/clone_1lb="CIT-HSP"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelBAC11; Site_1: HindIII; Site_2:
HindIII"
BASE COUNT 94 a 107 c 72 g 132 t
ORIGIN
Query Match 1.9%; Score 389; DB 90; Length 405;
Best Local Similarity 97.5%; Pred. No. 1,4e-34;
Matches 395; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Oy	9913	catgttgccaccacacacacttcagccttgcgtyggcaagtaagaacctttccaagaaga	9972
Db	405	CATGATGGCCACCACTTACACTTGAGGTGCAGATAAGACCCTGTCTCAAAAGACT	346
Oy	9973	acaagaaaaaaagaaaataattttttaaaagtgtggcgcaagaaagatactaataag	10032
Db	345	TCAAGCACAAACAATAGAACAATTTTAAAAAGTGGGGCCAGTAACATCTGAATAG	286
Oy	10033	gcacatcaagacacactaagaanaactctgatgaagttctagaaccgaaggatgtaga	10092
Db	285	GCACATCAAGACACACTACTAAGAAATCTGACGAACTCAGACCGAGGGAATGATGCAGA	226
Oy	10093	tgtcagaagttcacagatatgaagaagaggttacttacgaftccagttctttggagatccact	10152
Db	225	TGTCCAGAGTTTCAGATAGAAAGAGGATTACTTACAGATCCAGTTTTTTGGAGATGCACCT	166
Oy	10153	cacattgagttcaaacacacagatcttgttggagaatgctgttaagctctgtaactgaccaatgac	10212
Db	165	CACATTGAGGTCAAGACAGATCTTTGAGATGTCGTTAGCTGTACTGCCAACATGAC	106
Oy	10213	aatgtaagttggtgttcccgttcttatttaagggcccttgcaactgtgacacgggaatttacc	10272
Db	105	AATGATGGTGGTGTCTCTGTTCTTTATTACGGCCCTGGACCTGCACAGGGAATGTTAAC	46
Oy	10273	gaagggacacagggacataatgatgaataagaaagagtcggat	10317
Db	45	GAAAGGACACAGGACCATATGATGATGAATGGAAGATCCGGAT	1
RESULT	9		
AA251874			
LOCUS	AA251874	422 bp mRNA EST	13-AUG-1997
DEFINITION	zs10h11.f1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684837 5'		
KEYWORDS	AA251874	mRNA sequence.	
VERSION	AA251874.1	GI:1886854	
SOURCE	EST.		
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheraia; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 422)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	On May 18, 1995 this sequence version replaced gi:810999. Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LLNT ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 889 Std Error: 0.00 Seq Primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 372. Location/Qualifiers		
FEATURES			
source	1..422		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_image="IMAGE:684837"		
	/clone_id="NCI_CGAP_GCB1"		
	/tissue_type="germinal center B cell"		
	/lab_host="DH10B"		
	/note="Vector: pUT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD+), provided by Dr. Louis M. Staudt (NCI). Dr. David Allman (NCI) and Dr. Gerald Marti (CEBR). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTCCCAATCTGATGAGGAGGAGGCGGCTCATTTTTTTTTTTTTTTT-3'] . Double-stranded cDNA was ligated to Eco RI adaptors		

BASE COUNT	146 a	81 c	77 g	118 t
ORIGIN				
Query Match	1.98;	Score 386.8;	DB 30;	Length 422;
Best Local Similarity	94.8%;	Pred. No. 2.4e-34;		
Matches 400;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;
QY 19473	taagtttaacattaaacaacacatatataaagaaataattagcttctcgtatataaa	19532		
DB 1	TTAAGTTTAAACATTAAACAACACACTAATATTAAGTAAATTTAACTATCTGGTATTA	60		
QY 19533	atcacacaagaagtaattataataataaatygttctagcttctctgtcctaaact	19592		
DB 61	ATCATATCAAGAAGAACTTTTAAATTAATTAATTAATTTAGCTTCTTGGCTTAA	120		
QY 19593	aataaataaggtcctaaaggaacatcattctactagagatcatagaagttaaac	19652		
DB 121	AATATAAATAGTGTCTTAAGGAAACATTCATTCTAGAGAGACATCAAGTTTAA	180		
QY 19653	ttaaaaacaacttgcgcaattaagacagcatcaccaagaatgcgaatgccttggt	19712		
DB 181	TTTAAACAAACTTTTGCAATTTAAGCGCATACCAAGATGCAATGCTGGTGAAT	240		
QY 19713	atcaaatatccatctgcacattaaacaaagcagttgtactgtgtgcacatgcag	19772		
DB 241	ATCATATTTTCATCATCTGCACGCTTAACAAAGCAATGTTATGCTGTGACGTG	300		
QY 19773	ccagagggccctcatctgtcccccctcactaaagtgtctccagtcacacagcg	19832		
DB 301	CCAGAGCGCGTGATTTGTCCCCCTTCACATAAGTGCTCTCCAGTCGACGAG	360		
QY 19833	tgcacgtgagctcctttccagagattcicacgcctgcagtaataagttcagc	19892		
DB 361	TGCATGCTGACTCTTTTCCAGGATTCTACAGCTGGAGTGAATAGTCAAGCT	420		
QY 19893	tc 19894			
DB 421	TC 422			
RESULT 10				
AA283144	473 bp	mRNA	EST	14-AUG-1997
LOCUS	ztl4d04.r1	NCI-CGAP-GCBI	Homo sapiens	CDNA clone IMAGE:713095 5',
DEFINITION	mRNA sequence.			
ACCESSION	AA283144			
VERSION	AA283144.1	GI:1926078		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 473)			
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
	Unpublished (1997)			
	On May 8, 1995 this sequence version replaced gi.801207.			
	Contact: Robert Strausberg, Ph.D.			
	Tel: (301) 496-1550			
	Email: Robert_Strausberg@nih.gov			
	This clone is available royalty-free through LNL; contact the			
	IMAGE Consortium (info@image.lnl.gov) for further information.			
	Insert Length: 999 Std Error: 0.00			
	Seq primer: -28ml3 rev2 EF from Amersham			
	High quality sequence stop: 450.			
FEATURES	Location/Qualifiers			
SOURCE	1..473			

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:713095"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTCACATCTGAGTGGAGCGGCGCCGTCATTTTCTTTT-
3'). Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

BASE COUNT 142 a 106 c 92 g 133 t

Query Match 1.9%; Score 380.8; DB 31; Length 473;

Best Local Similarity 90.9%; Pred. No. 1.1e-33;

Matches 431; Conservative 0; Mismatches 32; Indels 11; Gaps 2;

QY 19512 tttagctatctgtaataaatacatcagaagatattataataaattggttta 19571

1 TTTAGCTTATCTGTAATAAATCATACAGAAACATTATTAATTAATGATGTTTA 60

QY 19572 gcttctcttgcttaaaactaaataatagctcctaagaagaacattcatttactag 19631

61 GCTTCTTGTGCTTAATAAATAATTGCTGAAGAAACATTATTTACTAG 120

QY 19632 aggaatcagaagttaaagacttaaaacacttggcaattgaagacagatccaagat 19691

121 AGGATCTTAATAAGCTTAATAAACAATTTGGCAATTGAAGACGACCAAGAT 180

QY 19692 gcaaatgcctggtgtaaatgatcaaatcttcacatgcacattaaacaagaagctgt 19751

181 GCAAGTCCCTGGCTGAATGATCAATATTCATCTGCACTTTAAACAATGCAATTGT 240

QY 19752 tatgcttgacatggcagagagccctcattgtccccccttcaataaagtgtcc 19811

241 TAGCTTGTGCAATGAGCAGGACGATGATGTCCCTTCACATGAAGTGTCC 300

QY 19812 tccaagtcacagagcgtggcgtgcatgtacgtctttccagagattcagcctgagt 19871

301 TCCAGTTGACCAAGCATGGCTGACGGTAGCTATTTTCCAGGTTTCTACGCTTGGAGT 360

QY 19872 aataagtcacgcaaaactctctgccta-----tccctgtgggtcagcccccag 19921

361 AATAAGTCACGCAAGCTCTCTGCTATATCCCAAGTCCCTGCGGTAGCCCTGAG 420

QY 19922 ggcacatcagcctcgtctcccaacactaaagttcaacttcatgtctcagcaca 19975

421 GGCCGCGCAGCTTCCGTC-CCCAAGACTAAGTTCATTGCTGCTCATGCGCA 473

RESULT 11

LOCUS AQ277241 538 bp DNA GSS 22-NOV-1998

DEFINITION C17B1-E1-2522E11.TF C17B1-E1 Homo sapiens genomic clone 2522E11,

genomic survey sequence.

ACCESSION AQ277241

VERSION AQ277241.1

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 538)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building

JOURNAL Unpublished (1998)

COMMENT Other GSSs: C17B1-E1-2522E11.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/hungen/bac\_end\_search/bac\_end\_search.html.

Seq primer: M13-21

Class: BAC ends.

FEATURES

Location/Qualifiers

1. 538

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="2522E11"

/clone\_lib="C17B1-E1"

/sex="male"

/cell\_type="sperm"

/Note="Vector: pBeloBAC11; Site 1: EcoRI; Site 2: EcoRI; Caltech Human BAC Library D"

BASE COUNT 182 a 94 c 56 g 205 t 1 others

Query Match 1.9%; Score 373.8; DB 100; Length 538;

Best Local Similarity 85.5%; Pred. No. 5.9e-33;

Matches 465; Conservative 0; Mismatches 66; Indels 11; Gaps 4;

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538 TGTGTATATATTAAAGNATATGAGCCCTCGAATGTAACCTATTGAAGAAACAGTTT 479

QY 19108 atgtgcaagtgatagaagaagtaataatactcttggtaaaaaagattagaagggtca 19167

478 ATGTTAAGCGCGTGAAGAAAGTAATAATTAATCTTTGGTAAAGATTAAGAGGCA 419

QY 19168 taagaatgtagatttttactacatcaaaaggttaaaaaaattatgtttgaagtta 19227

418 TAAGAAATGAGATTTTACTTACATTAAAGTTAAAAA-----ATTGTTGAGGTTTA 363

QY 19228 agcaagttttaaaatgtaattgtaaaaaaaattcgtgtgttaaaactaattagctaaag 19287

362 AGCAAGTTTGAATGTATTTGT- AAAGGAATTTCTGTGTGAACCATATTGGCTAAG 304

QY 19288 ataaaaagttatcatcaattttctgtgaactgagcattaaagttaaatgcaaaagtt 19347

303 TTAAGGGGTGATCATCAATTTTCTGTGAACGTGACATTAAATAAGCAACAAGGT 244

QY 19348 tttcttgaagcacaacctgctctttaaacaataataaaggttaaaagagctgt 19407

243 TTTTCTTAAGTACTAAGTCTGCTTTTAAACAAAATTAATGAAGCGTTAAGAGGCTAT 184

QY 19408 aaaaacttaacctatgtcaacatgaaaaattgtaaaatagtctatagagtttatt 19467

183 AACAATTTTACCTTATGTCAGACATTAATTAATGATAATATGTCACAGATTTTATT 124

QY 19468 aaaaatgaatttaaacattaaacatacaataaaggttaaaatagcttaactgtgta 19527

123 AAAATTGAGTTTAACTATTATAGCACACTAATAATTAAGGTGAATTTTACTTATCGGTA 64

QY 19528 taaaaatcaacaagaagcattataataataaaggtgttagcttcttggtccta 19587

63 T-AAAATCACACAGGAGCATTAATAAATGAATGAGTGTGGCTTTCTTGGTTTAA 5



Oy	19588	aaac	19591	
Db	4	AAAC	1	
RESULT	12			
LOCUS	AQ316362/c			
DEFINITION	AC016362 579 bp DNA			
ACCESSION	AC016362			
VERSION	AC016362.1 GI:4047825			
KEYWORDS	GSS.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
AUTHORS	1 (bases 1 to 579)			
TITLE	Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P., and Venter, J.C.			
JOURNAL	Use of human BAC End Sequences for Sequence-Ready Map Building			
COMMENT	Unpublished (1998)			
	Other GSSs: RPCI11-107L20.TV			
	Contact: Shaying Zhao, William Nierman, Mark Adams			
	Department of Eukaryotic Genomics			
	The Institute for Genomic Research			
	9712 Medical Center Dr., Rockville, MD 20850			
	Tel: 301 838 0200			
	Fax: 301 838 0208			
	Email: hbeet@igrr.org			
	Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong			
	[pieter@igrr.org, med.buffalo.edu]. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html			
	Seq primer: SP6			
	Class: BAC ends.			
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	/db_xref="taxon:9606"			
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	/clone_lib="RPCI-11"			
	/sex="Male"			
	/cell_type="Lymphocytes"			
	/note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"			
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Best Local Similarity	84.7%; Pred. No. 1.1e-32;			
Matches	466; Conservative 0; Mismatches 73; Indels 11; Gaps 4			
Oy	19054	attgataattggaagtaataagagcctctagat-----actatggaagaacagttta	19108	
Db	579	AATGATATATTTAAAGTAAATTTGGGCTCCCTCAATGTANAACTATTGGAAGAAACACTTTA	520	
Oy	19109	tgtgcaagtgcatagaagaagtaataatactattggtcaaaagattagaagagcat	19168	
Db	519	TGTGCAAGTGTGTAAAGAACTAAATATTTACTTTTGTGTAAGAAGATTAAAGAGGCA	460	
Oy	19169	aagaatgtgagatttacctacattaaagggttaaaaaaattattggtttggaagttaa	19228	
Db	459	AAGAATATGATTTTACTTACCTACATTTAAAGGTTAAAAA---ATTATTTTAAAGCTTTAA	404	
Oy	19229	gcaaatgttaaatgttaattgtaaaaaaaattcgtgtgtaaacataatgctaaaga	19288	
Db	403	GCACGTTTGAACACTTAACCTGT-AATGGAATTTCTGTGTGTAAACATATTTGGCTAAAGT	345	

Qy	19289	taaaaggatcatccacgcttttctgctgaacggaacataaagctaaagctgacaggtt	19348
Db	344	TAAGGGTATCATCTCAAGTTTCTCTGTCACACGACATTTAAATTAAGACACACAGTT	285
Qy	19349	ttcttgaagcaccacacgctctctttaacaaaattataaaggttaaaagagtcgtga	19408
Db	284	TTTCTTAAGACCTACCTGCTCTTTAACAAAATATATTAAAGGTTTAAAGAGCTATA	225
Qy	19409	aaaactaccctatggtcaacaatgaaaaattgataaataatgctataggttttatta	19468
Db	224	AAAATCTTACCTTATCGTCAGGACATTAATATGATTAATATGCTACAGGCTTTTATTA	165
Qy	19469	aaattaagtttaacattataaacacacaaataaagtraaaattagttctcgtat	19528
Db	164	AAATTGAGTTTACATTTAATATACACACTAATATTAAGGATTAAGTTTATCTGGTAT	105
Qy	19529	aaaaatcacagaagatattataataaataatggttgcttgccttcttgctctaaa	19588
Db	104	-AAATCATACGAGAGATTTGTCAAATATAAATGATGTTTGCGTTCTTGATCTAA	46
Qy	19589	aactaataa 19598	
Db	45	AACAAATA 36	
RESULT 13			
AF101960	2971 bp	DNA	GSS 08-MAR-1999
LOCUS	Homo sapiens chromosome 11 clone PTMB59.14 map 11p15.5, genomic		
DEFINITION	survey sequence.		
ACCESSION	AF101960		
VERSION	AF101960.1 GI:4193786		
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 2971)		
JOURNAL	Bepler,G., O'Brian,K.C., Kim,Y.-C., Schreiber,G. and Pitterle,D.M.		
MEDLINE	A 1.4-Mb high-resolution physical map and contig of chromosome		
FEATURES	segment 11p15.5 and genes in the LOH1A metastasis suppressor		
source	region		
Genomics 55 (2), 164-175 (1999)			
99134294			
2 (bases 1 to 2971)			
Bepler,G., O'Brian,K.C., Kim,Y.-C., Schreiber,G. and Pitterle,D.M.			
Direct Submission			
Submitted (27-OCT-1998) Medicine and Radiology, Duke University			
Medical Center, Box 2610, MSRB, Room 117, Durham, NC 27710, USA			
Location/Qualifiers			
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/organism="Homo sapiens"			
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metastasis suppressor region Bln T"			
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Best Local Similarity	71.9% Pred. No. 1.9e-31;		
Matches 537; Conservative 0; Mismatches 200; Indels 10; Gaps 5			
Qy 5097 caaatcattactctgtatcttcttaaaaatgacactcttgcttgcttgctgtt			
Db 424 CAAAAAACCCACAGCAACATATATATATATATATATTTGTTATTTATTTATTT			
Qy 5157 tgttttttgagacaggtctccactccctgctggccagagctgagtgagagcttgatca			
Db 484 TATTTTCCGAGACAGTGTCTACT-CTGTTGCCAGACTGGAGTGCAGTGGCACAACTT			

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Db	543	TGGCTCACTGCACACTCCGCCCTCCTGGGTTCAAGGATTTCTGCTCTCAGCCTCCAG	602
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Db	603	TAGCTGGGATTAAGAGCGCCGCCACCAACACACACTAATTTTGTATTTTAGTAGAGA	662
QY	5337	tggggttttgcattgttgcacaggaagttctaaactccttgggtccgaagcatccgccg	5396
Db	663	TGAGGTTTCACAAATTGTGGCAGGCTGGTCTCAAACTCTGACCTC--GTGATCCACCA	720
QY	5397	cctcagagtcaccaagtaactggtatctagtggtgtggccacgtcaccccgcaacactct	5456
Db	721	CCTCAGCCTCCCAAGTGTCTGGGATTACAGGATTAAGCCACCGCATCTGGCC---CAAC	776
QY	5457	ctcatataactagatatagtatcaccttcaagaacttaacatttgltcggcacagtg	5516
Db	777	ATTATATTTTATGTGGAAGACTGAATGTTTCTTAAGATCAGAAACACGCGCACAGTG	836
QY	5517	gtcacgcctctgaatcccaagcatctttgggagccgagttggtgatctacaagtcaaga	5576
Db	837	GCTCAGCCTGTAACTCTGGCACTTTGGAGGCCGAGCGGGCAATACGACGAGCTACAGA	896
QY	5577	gttcaagacccacccctcggccaaagtgtgtgaaccccgctctctactaaaatgaatgaa	5634
Db	897	GATCAGACACATCCCTGGCTTAACACGGTGAAACCCCGTCTCTACTATAAATAATAA	956
QY	5635	aattagtcagcagtcgtgtgacgtttgcctgtatctcccaatactcggagctgaagc-ag	5693
Db	957	AATTAGCTGGGGTCAAGTGTGGGCACTGTAGTCCCACTACTCGGAGGCTGAAGCGGG	1016
QY	5694	agaattgcttgaaccccaagagcggaagctcgaatgaaaccaagatcgtgccaatgcactc	5753
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Db	1077	CAGCCTAGGCGACAGGCGGAGACTCCGACTCAAAAAAAGATTGAATGAATGAACA	1136
QY	5814	cttagcttactgttcataatcccaatt	5840
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RESULT 14			
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DEFINITION	AQ752136 866 bp DNA	GSS	19-JUL-1999
ACCESSION	HS_5571_B2_B12.T7A RPCI-11 Human Male BAC Library Homo sapiens		
VERSION	AK752136		
KEYWORDS	AQ752136.1 GI:5539294		
SOURCE	GSS.		
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
REFERENCE	1 (bases 1 to 866)		
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,		
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and		
	Hood,L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and		
	scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)		
MEDLINE	99380589		
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L		
	High Throughput Sequencing Center		
	401 Queen Anne Avenue North, Seattle, WA 98109, USA		
	Tel: (206) 616-3618		
	Fax: (206) 616-3887		
	Email: jwallace@u.washington.edu		

	<p>Clones are derived from the human BAC library RPc1-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPac Resources (<a href="http://bacpac.med.buffalo.edu/ordering_bac.htm">http://bacpac.med.buffalo.edu/ordering_bac.htm</a>) or from Research Genetics (<a href="http://www.hsc.washington.edu">http://www.hsc.washington.edu</a>). BAC end Web Server: <a href="http://www.hsc.washington.edu">http://www.hsc.washington.edu</a></p>					
	<p>plate: 1147 row: D column: 24 Seq primer: 17 Class: BAC ends High quality sequence stop: 866.</p>					
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	or from Resear h Genetics (Info@resgen.com).					
	plate: 1147 row: D column: 24					
	Seq primer: 17					
	Class: BAC ends					
	High quality sequence stop: 866.					
BASE COUNT	241 a 244 c 177 g 202 t 2 others					
ORIGIN						
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Best Local Similarity	72.3%; Pred No. 4.6e-33;					
Matches 612; Conservative	0; Mismatches 94; Indels 141; Gaps					
Oy 17606	ctgcctctgtggaacaaccctctctgtggaactccaacagccagagtacgcygatcctgag	17665				
Dd 864	CTTGCGCTGGGAGGATGCCCTTCGGGGGATCCGGGCACCTTGAAGAATGACAGATCCTTAG	805				
Oy 17666	agctctcctgtgttagcaattgcccggttggagaacctccgccaaggcagtgtygtgcagg	17725				
Dd 804	AGCACTCTCGGGGTAGGCAATTGCCCCCTGGT-GGACCCTCGTCAGAGCGGTGAACAGAG	746				
Oy 17726	ccccctgtgagagatacaagagttgtgtctaacaacgggaaaggaattgacactgtgaatccg	17785				
Dd 745	C CCTGTGTNATGATCAGTCAGTCAGTGGCTTAACAACCGAAGAAGAACTGGCATGAGAGTCCG	686				
Oy 17786	gacaactaaaacttgytaagactagtccttgygaacttgcacatccattgaagtgaagc	17845				
Dd 685	GACACTGTGAALCTTGTTGTAAGACTGGTCTTTGGAACTTCCCACATCCANTMGAGTGAAGC	626				
Oy 17846	atggcctgatatacccacggcggtgccttatcaagaacctggtttggtttgactggttt	17905				
Dd 625	ATGGCCTTATATCACCCACGAC-----	605				
Oy 17906	gaattacttgacagcactgctcttgbgaacttgcaccaatccatccatccactcatltgagt	17965				
Dd 605	-----	605				
Oy 17966	ggaagcattgacctgatctgatcaaccacgtygtgcctgtccgcgcaacttggtttgtt	18025				
Dd 605	-----GTGCGCTTACTGGGACCTTGGTTTTGTT	577				
Oy 18026	ttagcttgaacttgaattgcttgaacttgaattgtttgttttgaacttgccttgaattct	18085				
Dd 576	T TTGGCTTGACTTGATTCCTTGTAACCTTTGGTTTGGTTTGAACCTGCTTGAGATT--	518				
Oy 18086	gaatactctgatttbggttttgatttggttttagtgytaaacatgcacaaagtgtgtgcgtgc	18145				
Dd 518	-GATACCTCTGATTTTGG--TTGTTCTGTGGTTGGTGTAACGTGTAAGAAGTGNTGTGTC	462				
Oy 18146	ccttttcccgcttcttggtttttgggtgtgtcattgtgtgtgtgtgtgtgtgtgtgtgtgt	18205				
Dd 461	CCTCTTACCTGTTCTTTGTTTGGTGTGATGATGTGATGTGATGTGATGTGTTTGTCTG	402				
Oy 18206	gaagaaatatgtgtcaggcacaaaa-taagcccaacctctagaanaacttlyttaaaaaat	18264				
Dd 401	GAGGAACATGGGTGAGGACACAAGTGAAGCCCATCCACTGAGAACCTATGTTGAATAATT	342				
Oy 18265	tcaagaaagatttaagggaattaacggtgttactatgtaacactagaanaaacttgaactt	18324				
Dd 341	TCAAAACAGGATTTAAAGGAGACTATGAGT--TATATACCAACAAGAAACTTTAAGACTT	285				

QY	18325	ttgttaaatagacatgcacacattagaggttgggttgcacatagaagagctctgac	18384
Db	284	TTGTGTGAGATAGACTGTGGCCACGACATTTCAGGTACGTGGCCATCAGAAAGAAAGCTGAC	225
QY	18385	ggtccctgtttccaatgtatgtgcacaaagtaacctgttaagccaagacacacagaccgt	18444
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Db	164	TCCCGTA 158	
RESULT	15		
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LOCUS	AF101960	2971 bp	DNA
DEFINITION	Homo sapiens chromosome 11 clone pTMB59.14 map 11p15.5, genomic survey sequence.	GSS	08-MAR-1999
ACCESSION	AF101960		
VERSION	AF101960.1	GI:4193786	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2971)		
AUTHORS	Bepler,G., O'Brian,K.C., Kim,Y.C., Schreiber,G. and Pitterle,D.M.		
TITLE	A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOH11A metastasis suppressor region		
JOURNAL	Genomics 55 (2), 164-175 (1999)		
MEDLINE	99134294		
REFERENCE	2 (bases 1 to 2971)		
AUTHORS	Bepler,G., O'Brian,K.C., Kim,Y.-C., Schreiber,G. and Pitterle,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-OCT-1998) Medicine and Radiology, Duke University Medical Center, Box 2610, MSRB, Room 117, Durham, NC 27710, USA		
FEATURES	Location/Qualifiers		
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	/clone="PTMB59.14"		
	/note="part of a 1.4 megabase contig including the LOH11A metastasis suppressor region Bln T"		
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ORIGIN			747 t

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Db	839	AGCCACCTGGCTGG---CTGTCTGATCTTGAAGAAACATTCAAGTCTTTCACATATA	784
QY	5432	aacttaacattgtctcgggacagtgctcaagcctttaatccagaattttggagcg	5553
Db	783	ATATATATTGGGCGACATGCGGAGCTTATGCGCTTAATCCAGCATCTTTGGAGCGTG	724
QY	5553	agggtggtggtacccaagttccaggaagtccaagaacgctgtgccaagtggtgaaaccc	5611
Db	723	AGGTGGGTGATCAAGAGGTCAGAGATTGAGACCGCTGGCCAACTTTGAAACCTC	664
QY	5612	gtctctactaaatgtcaaaaaaattagtcagagcttggtggcagttgctttaatccca	5671
Db	663	ATCTCTACTATAAAT---ACAAAAATTAGCTGTTGTGGGCGGCGCTTAAATCCA	607
QY	5672	gatactcgggagctctgggcca-gagaattgtctgaacccaagaagcgggagctctcagta	5730
Db	606	GCTATTTGGGAGCGCTGAGGCAAGATTCCTTTGAACCAAGAGGGGAGGTTTGAGTGA	547
QY	5731	gccaaagatcgtgccaacgcgcactccagcgttgcgagacagtgctctcaaaaaaaaaa	5790
Db	546	GCCAAAGATTGGCCACGTGACCTCAGTCTGGGCAACAGATGAGACATCTTGCGGANA	487
QY	5791	agaat 5796	
Db	466	ATAAAT 481	

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OM nucleic - nucleic search, using sw model

Run on: February 29, 2000, 08:44:14 : Search time 20117.6 seconds

(without alignments)  
-3767.414 Million cell updates/sec

Title: US-09-339-352-7\_COPY\_15000\_39960

Perfect score:

Sequence: 1 tctatcatgaatgaatgca.....cttctatcatgaggatgtga 24961

Scoring table: IDENTITY\_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl.\*

Word size: 0

Number of hits that pass the threshold: 1642386

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2: gb\_da2:\*  
3: gb\_da3:\*  
4: gb\_da4:\*  
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6: gb\_da6:\*  
7: gb\_da7:\*  
8: gb\_da8:\*  
9: gb\_da9:\*  
10: gb\_da10:\*  
11: gb\_da11:\*  
12: gb\_da12:\*  
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39: gb\_da39:\*  
40: gb\_da40:\*  
41: gb\_da41:\*  
42: gb\_da42:\*  
43: gb\_da43:\*  
44: gb\_da44:\*  
45: gb\_da45:\*  
46: gb\_da46:\*  
47: gb\_da47:\*  
48: gb\_da48:\*  
49: gb\_da49:\*

50: gb\_pl3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24961	100.0	102258	11	HS295C6	297876 Human DNA s
2	3992.2	16.0	135305	11	HSJ1112D6	AL080317 Human DNA
3	3544.4	14.2	227567	42	AC008554	AC008554 Homo sapi
4	3494	14.0	79376	11	HS454G6	298750 Human DNA s
5	3159.8	12.7	7728	11	AF058907	AF058907 Homo sapi
6	3082.6	12.3	137413	42	AC011036	AC011036 Homo sapi
7	2884.2	11.6	116679	32	HSJ0636H5	AL121602 Homo sapi
8	2879.4	11.5	162921	33	HSJ603114	AL122001 Homo sapi
9	2783.6	11.2	191235	42	AC012487	AC012487 Homo sapi
10	2647.2	10.6	163738	42	AC009505	AC009505 Homo sapi
11	2644.2	10.6	138088	43	AC010877	AC010877 Homo sapi
12	2559.6	10.3	144304	32	HSJ0383P5	AL121947 Homo sapi
13	2414	9.7	105563	11	AC003983	AC003983 Human PAC
14	2396.8	9.6	37139	40	AC006047	AP006047 Homo sapi
15	2386	9.6	100000	10	AP000509	AP000509 Homo sapi
16	2385	9.6	236822	10	D84394	D84394 Homo sapien
17	2385	9.6	110409	42	AC010487	AC010487 Homo sapi
18	2343.6	9.4	158463	44	AC011019	AC011019 Homo sapi
19	2342.6	9.4	123585	11	AC004707	AC004707 Homo sapi
20	2328	9.3	18226	11	HS46618	AL030988 Homo sapi
21	2317.8	9.3	167932	41	AC008697	AC008697 Homo sapi
22	2296.6	9.2	161428	41	AC009542	AC009542 Homo sapi
23	2294	9.2	174768	40	AC009330	AC009330 Homo sapi
24	2286	9.2	113853	40	AF196971	AF196971 Homo sapi
25	2270.6	9.1	213315	43	AC016047	AC016047 Homo sapi
26	2215.4	8.9	36921	40	AC004185	AC004185 Homo sapi
27	2133.2	8.5	196501	40	AC005908	AC005908 Homo sapi
28	2096.8	8.4	171636	10	HS215K18	283820 Human DNA s
29	2089.6	8.4	246240	5	AR036572	AR036572 Sequence
30	2089.6	8.4	246240	5	AR036573	AR036573 Sequence
31	2089.6	8.4	246240	5	AR036574	AR036574 Sequence
32	1991.2	8.0	203488	42	AC009488	AC009488 Homo sapi
33	1991.2	8.0	173157	42	AC011895	AC011895 Homo sapi
34	1965.6	7.9	132805	11	HS339A18	297054 Human DNA s
35	1943.2	7.8	114330	40	AC004772	AC004772 Homo sapi
36	1868.4	7.5	226345	40	AC005406	AC005406 Homo sapi
37	1860.6	7.5	164285	42	AC009703	AC009703 Homo sapi
38	1709.2	6.8	268399	33	AC004469	AC004469 Homo sapi
39	1700.8	6.8	200607	44	AC016775	AC016775 Homo sapi
40	1589.4	6.4	112184	11	AC004054	AC004054 Homo sapi
41	1586.2	6.4	141672	10	HS142P18	AL031073 Human DNA
42	1556.2	6.2	179905	42	AC011751	AC011751 Homo sapi
43	1491	6.0	191079	33	HS1036D20	AL109851 Homo sapi
44	1470	5.9	158810	44	AC011604	AC011604 Homo sapi
45	1424	5.7	114638	11	HS799N4	AL022147 Human DNA

#### ALIGNMENTS

RESULT 1  
HS295C6 102258 bp DNA PRI 23-NOV-1999  
LOCUS Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains  
DEFINITION ESTs, CA repeat, STS and Cpg island.  
ACCESSION 297876  
VERSION 297876.1 GI:2582745  
KEYWORDS 1q24; Cpg island; repeat polymorphism.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 102258)  
AUTHORS Grafham,D.  
TITLE Direct Submission  
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Nov 2, 1997 this sequence version replaced gi:2465042.  
IMPORTANT: This sequence is the entire insert of clone 295C6.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variations annotated may not be found in the sequence submission  
corresponding to the overlapping clone as we submit sequences with  
only a small overlap as described above.  
This sequence was generated from part of bacterial clone configs of  
human chromosome 1, constructed by the Sanger Centre chromosome 1  
mapping group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1/  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key  
The true left end of clone 295C6 is at 1 in this sequence. The true  
right end of clone 295C6 is at 102258.  
295C6 is from the library RPCII constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong.  
For further details see http://bacpac.med.buffalo.edu/  
Location/Qualifiers  
1..102258  
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/db\_xref="taxon:9606"  
/chromosome="1"  
/map="1q24"  
/clone="RP1-295C6"  
/clone\_1fb="RPCT-1"  
891..1180  
repeat\_region repeat: matches 298. .9 of consensus"  
/note="AluSg repeat: matches 298. .9 of consensus"  
1375..1683  
repeat\_region repeat: matches 303. .1 of consensus"  
/note="AluSp repeat: matches 303. .1 of consensus"  
2028..2310  
repeat\_region repeat: matches 300. .1 of consensus"  
/note="AluSg repeat: matches 300. .1 of consensus"  
2612..2903  
repeat\_region repeat: matches 301. .1 of consensus"  
/note="AluSg repeat: matches 301. .1 of consensus"  
complement(4475..4866)  
/note="match: 223618 STS containing (CA) repeat"  
4625..4670  
repeat\_region repeat: matches 146. .60 of consensus"  
/note="23 copies of GT 100 & conserved; differs from  
223618"  
4766..4897  
repeat\_region repeat: matches 145. .1 of consensus"  
/note="MIR2 repeat: matches 145. .1 of consensus"  
4969..5140  
repeat\_region repeat: matches 1475. .1300 of consensus"  
/note="MIR42c repeat: matches 1475. .1300 of consensus"  
5146..5448  
repeat\_region repeat: matches 302. .1 of consensus"  
/note="AluJo repeat: matches 302. .1 of consensus"  
5503..5795  
repeat\_region repeat: matches 1. .299 of consensus"  
/note="AluSg repeat: matches 1. .299 of consensus"  
5797..5925  
repeat\_region repeat: matches 1265. .1124 of consensus"  
/note="MIR42c repeat: matches 1265. .1124 of consensus"  
5923..6039  
repeat\_region repeat: matches 920. .804 of consensus"  
/note="LIMB6 repeat: matches 920. .804 of consensus"  
6123..6415  
repeat\_region repeat: matches 1. .292 of consensus"  
/note="AluSx repeat: matches 1. .292 of consensus"  
7799..8099  
repeat\_region repeat: matches 302. .1 of consensus"  
/note="AluSx repeat: matches 302. .1 of consensus"  
9002..9302  
repeat\_region repeat: matches 2. .303 of consensus"  
/note="AluSp repeat: matches 2. .303 of consensus"  
9692..9983  
repeat\_region repeat: matches 1. .301 of consensus"  
/note="AluJo repeat: matches 1. .301 of consensus"  
10986..11071  
repeat\_region repeat: matches 146. .60 of consensus"  
/note="MIR2 repeat: matches 146. .60 of consensus"

repeat\_region repeat: matches 262. .70 of consensus"  
/note="MIR repeat: matches 262. .70 of consensus"  
12180..12479  
repeat\_region repeat: matches 1. .300 of consensus"  
/note="AluSg repeat: matches 1. .300 of consensus"  
13246..13500  
repeat\_region repeat: matches 256. .1 of consensus"  
/note="MIR repeat: matches 256. .1 of consensus"  
13907..13973  
repeat\_region repeat: matches 75. .141 of consensus"  
/note="MIR repeat: matches 75. .141 of consensus"  
13975..14489  
repeat\_region repeat: matches 526. .1 of consensus"  
/note="MIR repeat: matches 526. .1 of consensus"  
15702..16064  
repeat\_region repeat: matches 1. .371 of consensus"  
/note="THE1C repeat: matches 1. .371 of consensus"  
16144..16585  
repeat\_region repeat: matches 9. .466 of consensus"  
/note="MIR repeat: matches 9. .466 of consensus"  
17173..17534  
repeat\_region repeat: matches 105. .449 of consensus"  
/note="LIR2 repeat: matches 105. .449 of consensus"  
41786..421827  
prim\_transcript repeat: matches 105. .449 of consensus"  
/note="match: multiple ESTs; match: AA165668 C16515  
AA077391"  
18004..18120  
repeat\_region repeat: matches 39 mer 81 & conserved"  
/note="3 copies of 39 mer 81 & conserved"  
19377..19377  
prim\_transcript repeat: matches 105. .449 of consensus"  
/note="match: multiple ESTs; match: AA6026 H60052 H1282  
T62974 AA283144; match: T57835 F00049 N75628 AA382351  
AA300207; match: W37181 N52820 AA337459 W87851 H84729;  
similar to endogenous retrovirus POL POLIPROTEIN"  
422156..42928  
repeat\_region repeat: matches 788. .892 of consensus"  
/note="match: multiple ESTs; match: AA401243 AA258918  
AA248892 AA096209 R36280"  
23025..23060  
repeat\_region repeat: matches 105. .449 of consensus"  
/note="3 copies of 12 mer 94 & conserved"  
23519..23865  
repeat\_region repeat: matches 105. .449 of consensus"  
/note="LIR2 repeat: matches 105. .449 of consensus"  
24473..24785  
repeat\_region repeat: matches 1. .299 of consensus"  
/note="AluSg repeat: matches 1. .299 of consensus"  
25027..25058  
repeat\_region repeat: matches 1. .299 of consensus"  
/note="16 copies of 2 mer 88 & conserved"  
25877..25987  
repeat\_region repeat: matches 788. .892 of consensus"  
/note="LIR2 repeat: matches 788. .892 of consensus"  
26022..26312  
repeat\_region repeat: matches 1. .295 of consensus"  
/note="AluSg repeat: matches 1. .295 of consensus"  
26752..27050  
repeat\_region repeat: matches 1. .299 of consensus"  
/note="AluSg repeat: matches 1. .299 of consensus"  
28012..28312  
repeat\_region repeat: matches 1. .303 of consensus"  
/note="AluSg repeat: matches 1. .303 of consensus"  
28316..29066  
repeat\_region repeat: matches 109. .907 of consensus"  
/note="LIR2 repeat: matches 109. .907 of consensus"  
29517..29629  
repeat\_region repeat: matches 262. .151 of consensus"  
/note="MIR repeat: matches 262. .151 of consensus"  
29631..29928  
repeat\_region repeat: matches 1. .295 of consensus"  
/note="Alu repeat: matches 1. .295 of consensus"  
29937..30237  
repeat\_region repeat: matches 1. .301 of consensus"  
/note="AluSg repeat: matches 1. .301 of consensus"  
30238..30315  
repeat\_region repeat: matches 158. .76 of consensus"  
/note="MIR repeat: matches 158. .76 of consensus"  
31096..31287  
repeat\_region repeat: matches 56. .262 of consensus"  
/note="MIR repeat: matches 56. .262 of consensus"  
31289..31379  
repeat\_region repeat: matches 146. .56 of consensus"  
/note="MIR2 repeat: matches 146. .56 of consensus"  
31479..31525  
repeat\_region repeat: matches 146. .95 of consensus"  
/note="MIR2 repeat: matches 146. .95 of consensus"  
33069..33318  
repeat\_region repeat: matches 9. .253 of consensus"  
/note="MIR repeat: matches 9. .253 of consensus"  
33565..33744  
repeat\_region repeat: matches 262. .74 of consensus"  
/note="MIR repeat: matches 262. .74 of consensus"  
36165..36466  
repeat\_region repeat: matches 1. .302 of consensus"  
/note="AluSx repeat: matches 1. .302 of consensus"  
36692..36944  
repeat\_region repeat: matches 3. .240 of consensus"  
/note="MIR repeat: matches 3. .240 of consensus"  
36999..37299  
repeat\_region repeat: matches 301. .1 of consensus"  
/note="AluSg repeat: matches 301. .1 of consensus"  
37924..38114  
repeat\_region repeat: matches 1055. .866 of consensus"  
/note="LIR2 repeat: matches 1055. .866 of consensus"

repeat\_region 38108..38475  
/note="MSTR repeat: matches 426..1 of consensus"  
repeat\_region 38479..38657  
/note="LIMA2 repeat: matches 874..687 of consensus"  
repeat\_region 38658..38957  
/note="LIM3 repeat: matches 300..1 of consensus"  
repeat\_region 38958..39580  
/note="LIM3 repeat: matches 699..85 of consensus"  
repeat\_region 39385..39875  
/note="LIM3 repeat: matches 292..1 of consensus"  
repeat\_region 39877..39951  
/note="LIM3 repeat: matches 88..14 of consensus"  
repeat\_region 39944..40919  
/note="L1 repeat: matches 4416..5390 of consensus"  
repeat\_region 40769..41662  
/note="L1 repeat: matches 1..893 of consensus"  
repeat\_region 41764..42556  
/note="L1 repeat: matches 5133..4305 of consensus"  
repeat\_region 42557..42857  
/note="L1 repeat: matches 1..301 of consensus"  
repeat\_region 42876..43925  
/note="L1 repeat: matches 4313..3215 of consensus"  
repeat\_region 44235..44498  
/note="MERA3 repeat: matches 3..272 of consensus"  
repeat\_region 44788..44860  
/note="MIR repeat: matches 154..82 of consensus"  
repeat\_region 44933..45220  
/note="LIM3 repeat: matches 289..2 of consensus"  
unSURE repeat\_region 45304..45336  
/note="LIM3 repeat: matches 1..301 of consensus"  
repeat\_region 45337..45637  
/note="LIM3 repeat: matches 1..301 of consensus"  
repeat\_region 45934..46220  
/note="LIM3 repeat: matches 302..14 of consensus"  
repeat\_region 46817..46935  
/note="MIR repeat: matches 35..154 of consensus"  
repeat\_region 47393..47677  
/note="MIR repeat: matches 1..302 of consensus"  
repeat\_region 48309..48404  
/note="MIR repeat: matches 48..140 of consensus"  
repeat\_region 48620..48862  
/note="MIRA1B repeat: matches 347..102 of consensus"  
repeat\_region 48865..49159  
/note="LIM3 repeat: matches 1..296 of consensus"  
repeat\_region 51182..51467

Query Match 100.0%; Score 24961; DB 11; Length 102258;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 24961; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcttttcaatggaatgcaataatccctgttctgtgagaataatcaagaagaagaagt 60  
| | | | |  
Db 15000 TCTTTTCAATGGAATGCAATAATCCTGTTGTGAGAAATCAAGAAAGAGAGT 15059

QY 61 tttaataatataatggaataatagaggttgaagaagagctgtctctatatt 120  
| | | | |  
Db 15060 TTTTAAATATATATTTTGAATAATATAGAGGTGAAGAAAGCTGCTCTCATATT 15119

QY 121 cagcataatagatgagatttccaagctatctgcgaatggttcttattgtctctg 180  
| | | | |  
Db 15120 CAGCTATATGATGAGATTTCCTCAAGCTATCTGCAAGGTTCTTATGCTGCTTG 15179

QY 181 atataatcccttctctgttcccaagcccgatataattactagtaattctctcc 240  
| | | | |  
Db 15180 ATATATCTCCCTTCTCTGTTCTTAAGCCCTGATTAATTAACCTAATGCTATCTCC 15239

QY 241 ttctcagctcctactgcaaccctactactcaacaatagcaagccactaccatcaagt 300  
| | | | |  
Db 15240 TTTTCAAGTCTACTGCAACCTATATACCAATAGCAAGCACTACCCCATCCAGGT 15299

QY 301 catgaacctctgactggagctcccatctgctcaagcgcaatgaaccaggctccttattg 360  
| | | | |  
Db 15300 CATGACCTCTGACTGGAGCTCCATTCCTTAAGGATGAACCAAGCCTCTCTTATG 15359

QY 361 tgacacaaagacttccaagaagcctcattctatctcttctgtcagctctgcttagca 420  
| | | | |  
Db 15360 TGACACAAAGACTTTCCAAAGCTCATTTCTCTTCTTCCACTCTCTCCATGCA 15419

QY 421 tctacccttccaaacagcaagctagaggttccctgtcacaccagagctattctcc 480  
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Db 15420 TCTACCTCTTCAACAAAGCAAGAGTGAAGTTCCTGCAACCAAGAGATTTTCTCC 15479

QY 481 tctcagcttctgttctatgctctctcctcagccagagtgctatgcttctcattgcc 540  
| | | | |  
Db 15480 TCTCATGCTTGTGCTTATGCTGCTCTCCACAGCCAGAGTGTATGCTTCAATGGCC 15539

QY 541 ctcattgaggttcatctccaagctcagctcaggtggtgctcccggaacctgcatca 600  
| | | | |  
Db 15540 CTCATTGAGGTTCATCTCAATCTCACCTCGGTGAGCTCCGGAACGTATCA 15599

QY 601 tgcctaaaggttactacataacccttctctctgtaacttccacaattctctatgcatg 660  
| | | | |  
Db 15600 TGTCTAAGTTGACTATACCTATCCCTTTCTCTCAACTCCACAATCTCTATGCTATG 15659

QY 661 actctacgttgcctcctacatataatcaactttaagtctatctgatactgctctg 720  
| | | | |  
Db 15660 ACTCTATGCTGCTCCCTCACTATATCACTTTATGCTATGATGATGATGCTGCTG 15719

QY 721 tgcctcaccacaaatctaatcccgatgcaaccccgagtgctcagggagagacgttt 780  
| | | | |  
Db 15720 TGTCTTCAACCAATCTATCCCTGATGCAACCCCAAGTGTCAAGGGAGAGACTGTT 15779

QY 781 gggaaagtatgatacagaaggggttcccccaatgctgtctcattatagatgagag 840  
| | | | |  
Db 15780 GGGAAAGTATGATGATGATGAGGGGCGGTTCCCCATGCTGTTCTATGATGAGGGAG 15839

QY 841 ttctcatgagattgatgtttaaagtttggacattccctccctgtcgtctctctctg 900  
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Db 15840 TTTCTATGAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 15899

QY 901 ccacatgtaagaactgcttctctccctctctctctctctctctctctctctctg 960  
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Db 15900 CCACATGTAAGAACATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 15959

QY 961 aggcctccctacagctgagaaactgtgagcaatgaacccctctctcttataaattacc 1020  
| | | | |  
Db 15960 AGGCTCTCTTACCATGAGTGAAGCTGATGATGATGATGATGATGATGATGATGATG 16019

QY 1021 cagttctcagtagttctcttataagcagcgatgaagaacagtaacaattctctctcc 1080  
| | | | |  
Db 16020 CAGTCTCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 16079

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| | | | |  
Db 16080 TCTTCTGTGAGAGCTCTTGAAGGCAAGAGCACTTATGATGATGATGATGATGATGATG 16139

QY 1141 acttgtgacacatgtccccaattctatgtaattctctagcctctagggcctcaaa 1200  
| | | | |  
Db 16140 ACTTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 16199

QY 1201 gtgtgaccttatttgaagaagagtcgttgcagatacaaatagttgaatgaatcagtc 1260  
| | | | |  
Db 16200 GTGTGACCTTATTTGAAAGAGAGTGTGCAAGATCAATTAATGATGATGATGATG 16259

QY 1261 tagagtaggtaggagcttcaatcaataaactgtgtgccttataaagaaggaatttg 1320  
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QY 1321 gacacaaacacacacaggaagatgcatgtgaatgaagcagagatgaagtgagcgc 1380  
| | | | |  
Db 16320 GACACAAACACACACAGGAGGAATGCCATGATGATGATGATGATGATGATGATGATG 16379

QY 1381 ttctcagaagcaatcttggaaacacaaagatggcagcgaacacacagaagcttagcagtg 1440  
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Db 16380 TTCTCAAGGCCATCTTTTGAAGACACCAAGATGGCCAGCAACACAGAGATGAGGTG 16439

QY 1441 ggcataaagacatctctcccatatgtctcagagaagaagaagatgcttgcctcagactc 1500  
| | | | |



Db	16440	GGCAGAAACAGATTCTTCCATATGCTCCAGAGAAAGATAGCTTATCTCAGACTC	164939
Qy	1501	ctacccttgagaaactatgagacaatcttcgtgtgtaagccatccatcttgtagtactttt	1560
Db	16500	CTACCCCTGAGAACTATGAGCAAAATTTCTGTTGTAAGCCATCCATTTTGTACTACTT	16559
Qy	1561	tacaaagcccgctagtagaataagacacttagtagtctccgaacatagttagattca	1620
Db	16560	TACAGAGCCCCGGCTAGTAAGATACGCCTTAGTAGTTCCTGAACATAGTAGAATTA	16619
Qy	1621	attaatgatitgatacatgatataaacaatgtctctcgtatctgtgtaattacccctca	1680
Db	16620	ATTATATGATGTAATACATGAATTAACAAATGCTTCTGTGACTGTGTGATATCCCTTA	16679
Qy	1681	gcattgataaagatatctttaaactcgcctctccagccctaaactttaatgtggataga	1740
Db	16680	GCAATGATTAAGATATTTTAAACAGCGCTTCTCAGGCTCAACTTAAATGTGGGATAGA	16739
Qy	1741	gataagccaagaatatattaagaattaaagaacattccctccacactggttaggttag	1800
Db	16740	GATTAAGCTTAACAAATTTTAAGATTAAACACATTTTCCCTCACACTGTTAGTTAG	16799
Qy	1801	gtcgggaagaggaatagagtcaccatcatattgtcctgtgtcatccacactgtatgaaat	1860
Db	16800	GTGGGGAAGGAGTATGAGTACCACTCATATTTGTCTGTGTATCACAACATGTTATGAAT	16859
Qy	1861	accatactatctacttccatgtggaagtgaatgatatgtcccaagaatagccctcataa	1920
Db	16860	ACCAATACATATCTACTCTCCATGTGGGAAGTAGAATGATTTGTCCAAAGATAGCCCTCATTA	16919
Qy	1921	tatctcctatagaaataataaacaacatgagaacaagtatatagatctgtctccag	1980
Db	16920	TATTCCTTATAGAAATATAAATAACACATAGACAACTATATATAGATCTGTCTCCAG	16979
Qy	1981	ggaaaaatccaagaacctcttatactctacagctcttagaactaaatggtttgaact	2040
Db	16980	GGAAAAATCCAAAGACCTCTTATTTCTCTATCTCCAGCTTAGACATAAATGGTTGAAC	17039
Qy	2041	agtgtctccctttgaagggaagaagaagccctccatattgtttatctaaagaag	2100
Db	17040	AGTGAATCCCTTTGAGGGAAGACAGACCTCTCATATTTGTTTATCTAGAAAGG	17099
Qy	2101	aaagaagaagtgaatattaaagcagaatagccgcgcctcgaagacaagaccgaaaccag	2160
Db	17100	AAAGAAGATGAATTAAGGACAGATAGCCCGCGCTTAGAACACAGACCGAACCAAG	17159
Qy	2161	cctgggcctgcctgacctaagctcgtgtgttaaatctgaacccctgcacttagcaactgt	2220
Db	17160	CTGTGGCCCTGCTGACCTTAAGCTCGGTATTAATAATGCACCCCTTGACCTTACCACTG	17219
Qy	2221	gttactctatagattccagacatctgtatgtaagagcatcttaltgaaagacatctgaaat	2280
Db	17220	GTTATCTATAGATTCACAGCATTTGATGGAAGGCAATTGTATGGAAGCATTTGGAAT	17279
Qy	2281	ctctcgtctctgttctggtttcaactgtgacacccggtgtctcaagccctgttaacgtaaccc	2340
Db	17280	CTCTGTCTCTGTTCGTTTCATCTGTGACACCGGTCCTACAGCCCTTACAGTACCC	17339
Qy	2341	ctggtcttcaatcatgatacagaacctctcagctgcgcgaaccccttagagtgtgacccct	2400
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Qy	2401	aaaagggacagaaglttagcatcagaagcgtcgaattttgagacgctagcctgcogatt	2460
Db	17400	AAAAGGACAGAGATGTGACATACAGCGAGCTCGGATTTTGAAGAGCTGTGCCCTCGGAT	17459
Qy	2461	ctccagactgataaagccaaccccttcaactctccggtgtctggaagggtttgtctcgg	2520
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Qy	2521	gtctactcgtctacattctctgttccctcgaacccggaagcaaggtgattaaacagatgttc	2580

Dd	17520	GCATTCCTGCTACATTTCTTGTTCCCTGACCGGGAAGCAAGGTATTAACAGATGTC	17579
Qy	2581	gaagcagctcctctaaagcggtcttagctgcgcctgtggaacatccctgctgggaattccaa	2640
Dd	17580	GAGGAGGCTCCTTAAGCGCGCTTTAACCTGCGCCTGTGGAACTCCCTGCGGGACTCCAA	17639
Qy	2641	ccagccagatgtagcggatcccttgagagctctccctgggttaggcatcttgcccggtgggac	2700
Dd	17640	CCAGCCAGAGTACCGCGGATCCTGAGAGCTCCTGGGTAGGCATTGGCCCGGTGGAC	17699
Qy	2701	acctgcagagcagtggtgtggaagccccgtggagaatcaacagagtgctgaacacc	2760
Dd	17700	ACCTGCCAGACATGTTGTGGCAGGCCCCCTGGAGAGATCAACAGAGTGTGAACACC	17759
Qy	2761	gggaaggaattggaacttggagatccggacaataaacttgtagactgaagctttgga	2820
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Qy	2821	cttgcccaactccatttgtagtgaagaatgctgcgtatcacccacggcgctgcttaaac	2880
Dd	17820	CTTGCCCACTCATTTGAGTGGAAAGCATGCGCTGATACCCAGCGGCTCTTATACAC	17879
Qy	2881	acttggtttggcttttgacttggttttgaaatcaacttgaacagacatggtcctgggaactgc	2940
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Qy	2941	ccacccacttccacttcaattgagtggaagaatggccgcatctgatacccaagatgtg	3000
Dd	17940	CCACTCATATCCCATCTCATTGTAAGTGAAGCATGGCTGATCTGATCCACCAAGGTG	17999
Qy	3001	ccgtgtccggcactcttggttttcttgcttgacttgaatctgctgatacttggt	3060
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Qy	3061	ttggttttgacctggtcttggatcttctgaactctgatttggttttgatttggtttg	3120
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Qy	3121	tgtaacatgcaaaagtgtgtgtgcgcctcttcaaccgtctcttgcttgggtgtgcat	3180
Dd	18120	TGTAAATGCAAAATGTGTGGGTGCCCTTTTACCCTTCTTGTGTTGTGTGTGACAT	18179
Qy	3181	gtgtgtgtgagatggtgtgttgtgtctcgaagaacaatgggttcagcacaataagccacc	3240
Dd	18180	GTTGTTGTAGATGTGTGTTTGTCTCGAAAGAACTAGGTGCTCAGGCAAAATTAAGCCAC	18239
Qy	3241	ctactagaacactgtttaaataattcaagaagaatttaaggagattacggttact	3300
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Qy	3301	atgaacatagaaaaacttagaaacttgtgtaaataagacttgcacaaatlaaggttgggt	3360
Dd	18300	ATGACACTAGAAAACTTAGAACTTGTGTAAATAATAGACTGSCCAATTAAGAGGTGGT	18359
Qy	3361	tggcatatagaagaagcttagacaggtgcctctgtttaaagtgtatgtagacaagttaac	3420
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Qy	3421	tgtaaagcaagacacacagacagatcttctgtacgtatagaacaattacagcttggtttagacc	3480
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Qy	3601	agagagaatatccaaagttagttaagaanaaaatagtgtaacctattcccttaaaagcca	3660
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Oy	3661	agtaaatctaaacctaaatctgtaatactaaaggtatcttcgtaacctctaaacac	3720
Db	18660	AGGTAAATTTAAACCTTAATATGATTAATTAAGGATATCTCGTAACCTGTAAACATC	187139
Oy	3721	taataccactctgtcttagtctgtaaacaaagggcgtatcccgaaagcactagcgctctc	3780
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Oy	3781	atcaaaatcccttaaccccgctaccacaggaatggcccaatcatctcaatctcgtacac	3840
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Oy	3841	agctcctctgcttaacaggaaaaaaaaagaagctctgtggaaagccaattctgtga	3900
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Oy	4021	gaaacagatgttataaaaaattatgcaaaaaatatgtataatctgaaagtaataagc	4080
Db	19020	GAAAAAGATGTTATAAAAATTTATGCAAAAAATATGTATATTGGAAGTAATAGGC	19079
Oy	4081	ctccgagctactatcgaaagaaacagcttctatgtgcaagctgcaataaagaftaaata	4140
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Oy	4141	cttttgttaaaaaagatlaagaaggagcabaagaatgtggaatttctacataaaagg	4200
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Db	19380	AAATTTATAAGGTTAAAAAGGCTGTAAAAACTTACTTATGTGTCAACATGAAAAAT	19439
Oy	4441	tggaataaatatgtctatggaagcttcttaataaaatlaagtttaacatataaacactaat	4500
Db	19440	TGGATTAATATGTCTATGAGGTTTTATTTAAATTAAGTTTAACATTAATAACACACTAAT	19499
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Db	19560	AAATGTGTATTAGCTTTCTTTGTGTCTAAAAACTAATAAAAATAGGCTCTTAAGGAACAT	19619
Oy	4621	tcaattctactagagatcatatagaatctaaagcttaaaacaaacttggcaattaaagca	4680
Db	19620	TCAATTTACTAGAGATCTATAAGATTAAAGCTTTAAACAACACTTGGCAATTAAAGACA	19679
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Db	19680	GCATCCCAAGATGCAAAATCCCTGAGTGTGAATGATCAATAATTTCCATCTGCACTTTAAAC	19739

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QY	480.1	ctaagctgtctcccaatccaccagagcgtgagcctgcaltgtagctctttccagatctc	4860
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QY	481	acagcctvgagtaataagltcatgccaactctctctgtatactccctgtgtgctgagcccg	4920
Db	19860	ACAGCCTGGAGTATATAGTATCATCCAAATCTCTCTGCTATCCCGTGGGTACCCCCG	1991
QY	492.1	agggccatccagccctccgtctcccaacactaaagttaactaatgtctctccacagaga	4980
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QY	9841	aaaattgtttaaattcttctctggggagcttttaagtaaccatgyggttttcagtttcatt	9900
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QY	9901	tgaattagaagctctgagagaagatctcttaatactccatataatgatttaataagt	9960
Db	24900	tgaattagaagctctgagagaagatctcttaatactccatataatgatttaataagt	24959
QY	9961	gtagaanaacttgaatcttgcctatagatcaacaacccaagaaatlaagccaaggtctaaacc	10020
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QY	10021	ctaaagcttgttttttttgttttttgttttttgttttttctcaacacactagaagtaac	10080
Db	25020	ctaaagcttgttttttttgttttttgttttttgttttttctcaacacactagaagtaac	25079
QY	10081	atgtagacttatcaactaggaaataaattatnaagttaggttctccatactaaacaat	10140
Db	25080	atgtagacttatcaactaggaaataaattatnaagttaggttctccatactaaacaat	25139
QY	10141	tatgataaanaatttttattcttgcattcctgttgaataaagaaaatttgcctcctgtataat	10200
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QY	10201	aagattactactaaatccagggtctacaaaagcattaccaggagataaattcaatttgcct	10260

Db	25200	AGATTATCTTAATTCCAGGGCTACAAAAGCATTTCCAGGGATAAAATTCATTGGCT	25255
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Oy	10321	gatttaggtttttctgtgtttaaacaacaatgatcgtctgtgagaataatgtaaaa	10380
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Oy	10381	cttggaaaagaaaaataaaaaatcaaccttgggtttcaacccctatcttctgtgtgt	10440
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Oy	10441	tttaaatctgttaacagcccttgggtgtgaaatctgaaaacctgtctgaagagctgtgaaa	10500
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Oy	10501	ttgtaatcttctgaagcgtgaggaatcttcgttcaaaaaagtgtgagactaatgtagagcta	10560
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Oy	10561	actattcctctgtgtctgtggcagatgaatgttggaggcccatcttgttatcctgataga	10620
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Oy	10621	acaaataaatcccggttatctcaatgtctcttgttgaagacataatccaagtta	10680
Db	25620	ACAAATAAATATCCAGGTTTATCTAATGTCCTTGTGGAAGACCTTAATTCAACTGTA	25679
Oy	10681	gacatttataaaaaagaaagcctaagtcctcttggctgtgtataatacttctgtgaatggtc	10740
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Oy	10741	tagtgaagaactccttagcagactgtatgtctctcttgggtgaabaatcccttcga	10800
Db	25740	TAGTGAGAACTCTTAGCAGACTGTATTCCTCTTTGGGTGAATAATTCCTTCTCTGAA	25799
Oy	10801	aatgcatcttgaaccccaattcttgtagaatgttttggtttcttggcctgaatgaagc	10860
Db	25800	AATGCATTTGAAACCTCAATTTGCTGAGATGTTTGTGTTTTCTTGGCTCAATGAAGAC	25855
Oy	10861	tcacataggaacttgaagaatgaggtcttcaaaagctgcaatgctgacacccaatgtga	10920
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Oy	10921	catgtatacatatgttgaacaacctgcagctgtgtgcatgtgttaacctagaacttaagta	10980
Db	25920	CATGTATACATATGTGAACAACCTGCACCTTGCTGTGATTTGTACCTTAACATTTAAAGTA	25979
Oy	10981	taataataaaaaataataatacaaaaaatacaaaagtcttccaggtctggagcgtgtgctc	11040
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Oy	11041	acgctgttaatcccaagcaactttgggaagccgaagccgggtgtgataccctgagttcaagagt	11100
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Oy	11101	tcgagacccagctcacaactgtaggaaaaccccgctcattataaaataacaaaatttagccgg	11160
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D	26640	AATCTGTGTTTGGTTATGTAGCTTGAAGAAAGGTATGTGACCTGTATCTTATGTCACTACT	26699
Q	11701	ggttgatatacagtgcaaaagggaacttagatcagatctgagaaatatatacatagtggtcac	11760
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Q	11821	tcaaggaattcaagaccagcctgtgccaataatggttgaaccccgctctctactaaatacaa	11880
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Q	11941	aagaatcgccttgaaaccgggaagcagaaaggttgaatgagcttgagatcgcgcacactgcact	12000
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 1 (bases 1 to 135305)  
 Direct Submission  
 Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humuqey@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk  
 On Sep 6, 1999 this sequence version replaced gi:5791529.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 EMBL, EMBL; SWISSPROT, Tr.; TrEMBL, Wp.; WormPep, Information  
 on the WormPep database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence is  
 the entire insert of clone 112D6. This sequence has been finished  
 according to sequence map criteria as follows. An attempt is made  
 to resolve all sequencing problems, such as compressions and  
 repeats, but not necessarily within known annotated human repeat

sequence elements (e.g. Alu). Where the sequence is ambiguous, this is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>

113D6 is from the library RPI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR>. PCYPAC2.

## FEATURES

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BASE COUNT 41171 a 26002 c 26091 g 42041 t

ORIGIN

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D	b		31904	G T A A A A T A C C T T A G T A A A A A A G A T T A A A A G A G C A T A A A A A T G G A T T T T A C C T A	31845
Oy			4191	c a t t a a a a g g t t a a a a a a t t a t g t t t t g a a a g t t t a a g c a a g t t t a a a t g t a a t	4250
D	b		31844	C A T T A A A A G G T T A A A A A A A T T A T T G T T T G A A A G T T A A G A A G T T T A A A T G T T A A T	31785
Oy			4251	g t a a a a a a a a t c t c g t g t g t a a c t a a t a g t a a g a t a a a a a g y t a c a t c c a g t t	4310
D	b		31784	G T A A A G A A A A -- T T C T G T G T O T T A A T A T T A C C T A A A A G T T A A A A G T V T C A C C A G T T T	31728
Oy			4311	t t c t g t g a c t g y g a c t t a a a g t a a a a t g y c a a a g g t t t c t t g a a c a c c a c t g c	4370
D	b		31727	T T C T G T G A A C T G C A C T R A A A T A A A A A A A A A A A G C A A C A G T T T T C T T A A A C A T C A A C I T C	31668
Oy			4371	t c t t a c a a a a a t t a t a a a a g g t t a a a a g a g t c t g t a a a a c t b a c c t a t b g t c a a a	4430
D	b		31667	T C T T T A C A A A A A T T A T A A A A A G T T A A A A A A G C T A T A A A A A T C T T A C C T A A T G T C A A A	31608
Oy			4431	c a t g a a a a a t t g a t a a a a t g t c t a g a g g t t t a t a a a t t a a g t t a a c a t t a a t a	4490
D	b		31607	C A T G A A A A A T T G A T A A A A T A T B T C T R A C A A G T T T A T T A A A T T A A T T T A A C A T T A A A	31548
Oy			4491	a c a c a c a t a b a a a a g g t a a a a t t a g c t t a c t g t a a a a a c a t a c a a g a a g t a t	4550
D	b		31547	A C A C A C T A T A T A A A A A G T A A A A T T T A A C C T A C T G T A T A A A A A A A C A T C A A G A A G C A T T	31488
Oy			4551	a t t a a t a a a a z i g t i t t a g t t t a g c t t c t t g t t o t t a a a a c t a a a a a t a a g t c c t a	4610
D	b		31487	A T T A A T A T A A A A A T G T G T T A G C T T T C T T A G T C T A A A A A A C T A A T A A A A A T T G T G C T A	31428
Oy			4611	a a g a a a c a t t c a t t t a c t a g a g a t c a t a g a a g t t a a a g a c t t a a a c a a c t t i g y c	4670
D	b		31427	A A G A A A A A C A T T C A T T T A C T A G A G A T C A T A A A A G T T A A A G A C T T --- A A A C T T T A C	31373
Oy			4671	a a t t a a g a c a g a t c c a a g a t g y c a a a t g c c g t t g t a a t a g a t g a c a a t a t c a t c a t c g	4730
D	b		31372	A A T T A A G A A G C A T A C C A A G A T G C A A A A T G C T G G T T G A A C G G A T C A A A T T A T T C A T C T G	31313
Oy			4731	c a c a t t a a c a a a a a g c a g t i g t a t g t c t g t g c a t a t g c a g c a a g a g c c c a t i g t	4790
D	b		31312	C A C G T T A A A C A A A A A C A A T T G T T A T G C T T G T G C A C A T G C A C C C A G A G G C C T G A T T G T	31253
Oy			4791	c c c c t c c a c t a a a g t y g t c c t c c a g t c a c c a a g c g t y g g c y c a t g t a g t a g c t c t t t	4850
D	b		31252	C C C C C T T C A C A T A A G T G T C C T C C A A G T C A G C A C A G C G T G G G C C T C A T G A T G A C T T T T	31193
Oy			4851	c a a g a a t c t a a g c t g a g a t a a d f c a t a g c a a a a c t c t g t g c a -----	4901
D	b		31192	C C A G A T T C T A C A G C C T G S A G T A A T A A G T C A T G C C A A G C T C T C T G C T A T T C C C A A A G	31133
Oy			4901	t c c c t g y g t c a g c c c c a g a g g c a t c a g c c t c g t c t c c a a c a t a a g t t a c t t	4960

D	31132	TCCTGGGGGTAGCTCCGGAGGGCATTCAAG6TTCCTCGTCCCAACATAACTTCACTT	31073
OY	4961	catgctctccacacagagaaacctagaattcccttgtagacctgaagtatgcaatg	5020
D	31072	CGGTCTCTCCACGGCTGGGAGAGACTTATGCAATTCCTTGGAGACTTAAAGGATGCAATG	31013
OY	5021	agcttaagaatttccaagagctatacaataagtcagccctggttcaccccccaagcgagtg	5080
D	31012	AGCTTAGAATTTTCAAGAGCTTATCAATCACTAGTCAGTCTTGTTCAATCCCTGATGGATG	30953
OY	5081	tgtgtgtagtattggtgtagaccttacttggcgactctgcccgaataacttgaatggcaact	5140
D	30952	TGTGGCAGTATGTGTGGTGAACCTTACTAGGACACTCTGTAATTAATTAAGTGGCACTT	30893
OY	5141	atacttaatgcagttggtgctatacccttccacccttggcatttcatacaacaagagggagaa	5200
D	30892	GTGCTTAGTCATTTGGGTATCCCTTACCCCTGGCATTTTCATCAACCCAGAGGAAGAA	30833
OY	5201	a-----aaataagatcgtataagcgagagaagccctctatagtcctt	5244
D	30832	AAATAATATATATATATATTAAGACATGCTAAGCAAGAGAG-CCCTTATAGTCTTT	30774
OY	5245	CGactctacgltccatttagacgcaatitggaatgccacgagagaataccagatcaatttaa	5304
D	30773	CAACTCCACATCTATTATTAGATGCAATTGGAGCCCGCCGAAGATATACATCAATTTAA	30714
OY	5305	agcttgaataccaatgctcacaaaaatttaagtaataatttaagagatga-tgtataata	5363
D	30713	AACCTGAATCAATATGTTACAGATTTTAAGCAATATTTTGGTAGATGACGTCATTA	30654
OY	5364	aaatgtaaatatagataaatatatacatatatacaacaacaacgaagaagctttcattagatt	5423
D	30653	AAATGTAGATTAATTAATACATCATCTATTATACCCCAACAGCAATGAATCTTTCATGATT	30594
OY	5424	-----gaaagaaaaactaaggtcggcccgccctggggctactgaacctgacgaagtgc	5480
D	30593	AAAAAAAACAACTATGTCGGCCCCAGCCCTGAGGCTACTCTGACCAAAACTCTT	30534
OY	5481	caactctgtgcgaaaaaaataaaaaaagaagcgacatctataccaattctaagtta	5540
D	30533	TGCACCTATAGT-----	30521
OY	5541	atttagactaacaaggtcttaccatagcaagaagataattgaatocccaacttacaag	5600
D	30521	-----	30521
OY	5601	gttttcaacaagaatgaagtgtcgtaaagaattaacagtgtaactgtattatagtaact	5660
D	30521	-----	30521
OY	5661	ctaatcttgtgccttagacagctctagtcacaagatataaagaagaagttcaactaaaaaa	5720
D	30521	-----	30521
OY	5721	aaaaaaaaaagaatggtatcttcaaaaaaataaaatgacgttgtaggttttaaccagac	5780
D	30521	-----GTCAAGAGGAAAAAATGCGACTTGGAGTTTAAACCCAGAC	30482
OY	5781	tgtatggctcttgcccaagcgccagttgacctctccaataaactagatgtygtttccaa	5840
D	30481	TGTAGGGCCCTGGCCAA-----GGCTATCTGTCAAAACAACTAGATGAGGTTTCAA	30422
OY	5841	agctgtgcccccatatacttaagggcccttgcagcaagcgccctgtttagcaaaagaacaga	5900
D	30428	AGGCTGGCCCCCATGTGCCAAGGGCCCTGTGTAGCATGTGCCCTGTATACAAAAAACAGA	30365
OY	5901	taagcttaactcttaggcaaaactaaacataaagtccccccaactgctgtgttgacttaa	5960
D	30368	TAAAGCTACTCTTAGCAACAACCTTAACATTAAGT-CCCCCAAGCTGTGTGATTTTAA	30310
OY	5961	tcaagtacaaaggacatactagctaatgaatgtctagataactatagataccaaagcttgc	6020
D	30309	TAAATACCAAGGACACCAATTAGTAAAGATGCTAGACTAAGTACAGATACCAAGCTTGC	30250



Qy	6021	tcgtgaaatcccccataaccatttgagtttgtaaacaccctaaaccgcgcacacttgc	6080
Db	30249	TCTGTGAAATATCCCGCATTAACCATGTGAAGTTTGCACAACCCCTAAACCCGCCACCTTAC	30190
Qy	6081	tcctggtatcagagagcccaagltaaacaataactgtgtgaagtgtgtgaactcaagttatc	6140
Db	30189	TCTCTGGTATCAGAGAGCCCAAGTTAAACATTAACCTGTGTGAAGTATTTGACATCAGTTTATT	30130
Qy	6141	cttagtgggcccacactccaaacacactcttaaacctcgtataactcgtgaagaggtgtgcg	6200
Db	30129	CTAGCAGGCCCAACACCCGGAACACCCCTTAACATCTGTGACTGGAGGATTTGACGTAAG	30070
Qy	6201	atggagagagcttccacaacactctgcaagtgactcaga-----aaagccctgttc	6252
Db	30069	ATAGAGAGAGCTTTGCCAACCCCTGTCAAAAGTGACTCTGAAGAAGACGACAAAGCCCCGCC	30010
Qy	6253	cagtcacacccggaaagtcagctgtcaccgcgcgcgaagcagcatgtagaacatcaacg	6312
Db	29949	GGACCCAAATTCCTTAAATTTGGACTTGAACAGTAAGAGACTCCACGTGACCTTCTTAG	29880
Qy	6373	actggaacctgtcccaqatatacatcaatcaagtcactgaggtagaacaaagattgctaca	6432
Db	29889	ACTGTAACCTGTTCCATATATATACATCAAGCAGCTAGAGTAGAGCAAAAGATTGCTACA	29830
Qy	6433	gtccctatatctcaltgattatataagtgtagcagaggaactctaaagaaacttgttgtat	6492
Db	29839	GTCCTATATTATTATGATTATTAAGTGTAAGCCGGACTCTAAAGAAACTGTTGTAT	29770
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Qy	6553	ccatttcaagccccaatgcatcacagcttctttaaataataaagagactgttccttct	6612
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Db	29649	AGGTATACACAAGTAAGTAATAGCTAGAACAGAAAGAAAGAGTCCCAAAATATGTATAC	29590
Qy	6673	actaaatttaatgtctgtgcacatcataatagcaatcgtgcataagaataagatgsgtgc	6732
Db	29589	CTTAAATTTGACGGCTGTGCGCTATTAAATAGTAACAGATGGGATAGGATGGGTTTC	29530
Qy	6733	tttaaacctgaaaaaaaaagttcacacagcaggaataaagatatactgcacagataa	6792
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Qy	6793	gtctcgtgcaaatgtgtgtataaatactcgtgcttgtgtcatcctaggtcctattagaagaag	6852
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Db	29416	ATAAATAATATCTGTTGGTCCCAAAAAAGAAATCATACGCCCTCTGTGCACAGTAG	29357
Qy	6911	aagctgcaacccttgaataatagtaatacaaatcccttaaaccgaagtgtgaaaaaag	6970
Db	29356	GAGCTGCACACCTTTAGATTTGATTAATACACAACCCCTCAGACCCCAAGTAATAAATAA	29297
Qy	6971	aagtaacgatatctctcgtggcgtgcataaaaaagagactagatctcagatlaaatacctag	7030
Db	29236	AAAGATATGTATACATTAGGCAATTGATGAAAAAGGACTGATCTCTGTATTAAGCAATCTTA	29237
Qy	7031	taaaagagagaggttcgtaaactctccggaaacagatattccaagcttctcatagttac	7090
Db	29236	TAAAGGAGAGGTTCAAAAGACGCTCTCCAGAACAGTATTTTCAGACTTTCTATGTATAAC	29177

QY	7091	taaatgfcgaagtaacccagagaccccaaggagaaaacccgaattgttttgcgaatgaacg	7150
Db	29176	TAATATGCGCAATACCTGAGATATCCAGAAAACATAAAATTTGTTTGGCAATTAGCG	29111
QY	7151	agcattgaagccagctctctaattgtaacctcaltgacgtttgttggagaaactgtaabaa	7210
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QY	7211	gagatcaatgg -cataagaagcccggaatttagtgcctcagaacccagttcctgtatgat	7269
Db	29056	GAGATCAATGCGCCATAGGAAGCCCGGAATTAGTTCCCAACACCCAGTCTGTATGAT	28999
QY	7270	tccgggcccgaagaataaccaccgtgcatctttcttgaagtttaagttccaatattagac	7329
Db	28996	TCCAGGCCCAAGAACACCCCTCGACAAATTTTAGTTTAAAAATCTCAATTATTAAGC	28933
QY	7330	aatactgcatagctgtaaaaaaggaagaattcactatcctgtlaagatgtaagttgccc	7399
Db	28936	AGTATTGCAAGCATTTGAAGGAAACAAATTCATCTATCTATAGGGCGGCTTAGTTC	2887
QY	7390	taggacaaaacactgtataatgttaccacaaaacagttacatgtgtggagtccaacaca	7449
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QY	7450	cagataaaatccattgaagaaattccaaagttgaaacggtttaagcccaaccaagat	7509
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Db	28756	TCCACCAAGACTGACAG -CCCCACCAAGTATATGTGATATGTGGACACAGACTTAT	2869
QY	7570	gctaagctgcttgacccagtgagacaggttagtgbtattgtgcaattaaacacatcttc	7629
Db	28697	TCTAAGCTGTGTGATCAGTGTGAGACAGGAGACTGTGATATGGACCATTAACCATCTTC	28633
QY	7630	ttcctactgcccatacaaaataggcgaactccgggcttcccgtctatagctttccggaa	7689
Db	28637	TTCTTACTGCCCCAATAAAGAGGTGAATCTTAGGCTTCCAGTATATGCTTCCATGAA	2857
QY	7690	aaggaacaactagcatagataattaaagaatgatgaatgacaccc -aaaaaattata	7748
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QY	7809	tacatgctcaactgtaatacatacaggttgcaagctgttttgaataatcaactaataaac	7868
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QY	7869	agtaagccttgatattcttggccggcgaagaacctcagataagaatgctatcatataa	7928
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QY	8047	gaactagttaaaaacatagaaaacactggacatagcccggttcgggtttagcaaggtatc	8106
Db	28217	GATATA-----ACAAACATGGGCACTATGCCGTGCAAGTGTAGCAGGATTC	2817
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Db	28169	AACCTGAAGCTATGTTAAAGTAGTGTCCAGCAGCTAGGAATTTTAAAACTCTTATA	2811
QY	8166	-ataggadttataagtaagaaacactgcttaactgctccctgcttgctgtgctgtact	8224

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Db 28109 AATGAGAGTATATATATATACTAAACCTGCTTACTGCTCCTGTTGTTGCTACTGACT 28050  
QY 8225 tcttgaatgataaaagctctgcttactgaagttcaccataatgcccacaacagt 8284  
Db 28049 TCTTCAAATGATAGAGCTTCAATCGCTACTTATGTTACACCAAAATGCTTACAGCACAAGT 27990  
QY 8285 gtaactatgaactactatcaatcattatgcacaagaagagcaagtgacaaataaag 8344  
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Db 27809 GAATATAATCAAAAGACAGCAGCCAGCGCCAGCCCAAAACCGGACCTGGGCTGCT 27750  
QY 8520 gaactaagcctggtagttaaatgcagccctgaacctgaactgtttatctatagat 8579  
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QY 8580 tccacacatgtatggaagagacattgtgaatcctcgtctgtcttctgtttcactgtgac 8639  
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Db 27629 CACCGGTGATGAGAGCCCGCTGACATACCCCTGTGCTCAATCAATCAGACACCTT 27570  
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Db 27569 TCAATG-TGAATATTTCATAGTCCCATGAGCCCTTAAAAGGACAGAAATGTGCCTGAGG 27511  
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RESULT 3  
AC008554/c LOCUS 227567 bp DNA HTG 31-OCT-1999  
DEFINITION Homo sapiens chromosome 19 clone CIT-HSPC\_513N18, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*, 100 unordered pieces.  
AC008554  
VERSION AC008554.2 GI:6165166  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 227567)  
AUTHORS DOE Joint Genome Institute.  
TITLE Unpublished  
JOURNAL Sequencing of Human Chromosome 19  
AUTHORS 2 (bases 1 to 227567)  
REFERENCE DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
COMMENT On Oct 31, 1999 this sequence version replaced gi:5686513.  
www.jgi.doe.gov.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 100 contigs. The true order of the pieces

\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
318: contig of 318 bp in length  
319: gap of unknown length  
886: contig of 568 bp in length  
887: gap of unknown length  
1782: contig of 896 bp in length  
1783: gap of unknown length  
2247: contig of 465 bp in length  
2248: gap of unknown length  
2470: contig of 223 bp in length  
2638: contig of 168 bp in length  
2639: gap of unknown length  
3193: contig of 555 bp in length  
3194: gap of unknown length  
3926: contig of 733 bp in length  
4631: contig of 705 bp in length  
4632: gap of unknown length  
5675: contig of 1044 bp in length  
5676: gap of unknown length  
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8501: contig of 509 bp in length  
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9192: contig of 691 bp in length  
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9921: contig of 729 bp in length  
9922: gap of unknown length  
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11570: contig of 653 bp in length  
11571: gap of unknown length  
12394: contig of 824 bp in length  
12395: gap of unknown length  
12821: contig of 427 bp in length  
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13086: contig of 265 bp in length  
13087: gap of unknown length  
13927: contig of 841 bp in length  
13928: gap of unknown length  
14388: contig of 461 bp in length  
14389: gap of unknown length  
14980: contig of 592 bp in length  
14981: gap of unknown length  
15641: contig of 661 bp in length  
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16503: contig of 445 bp in length  
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17470: contig of 613 bp in length  
17471: gap of unknown length  
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18896: contig of 671 bp in length  
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20001: contig of 1105 bp in length  
20423: gap of unknown length  
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21074: contig of 651 bp in length



[illegible]

Query	Match	Best Local Similarity	Score	DB	Length
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Db 201285	ACTCCAGAGTCGCCGCCACCATCTTGACACATGATGAGAGATGTCTCTAAACTTGGCC	201222			
QY 2046	ttccctgtttggaggagacagaccctctatttgtttatactcaagaaagga----	2102			
Db 201225	CCCTCTGGTGAAGGAGAGAACCCCTCATATTTGTTATTTGTTTATTACTCACTAC	201166			
QY 2102	-----aagaaaatgaattaaagga--gataccgcgcgccttagaaccagaccgcg	2152			
Db 201165	CTGTTTAAAGAAAAAACAGAGAGTGAATCAACAAAGACAGCACCCTGGCCAGGCCCA	201106			
QY 2155	aaaccaagccttgagccttcctgaactaaagctcgttagttaaattcgaccctgaactag	2212			
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Db 201045	AAATCAATGTATTATCATGATTCAGCA-----CAATTGTATAGAAAGAACAC	201001			
QY 2273	tgtgaatcctcgtcttcgtctcttcttaactgtgacacgcgttctcaagccctgtca	2332			
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Qy 2633	gactccaaacccgacgaatgtagcgcggaatccctgaagagctctctcgtgtgaagcatltgcgcc	2692
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Qy 2693	ggtggagacccctcgcagagcagtgctgtgagagggcccccgtggagagatccaaagatgagc	2752
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Db 200403	TGTATTGGACTTTGTTCTGTGGTTTGACTTGGCTTG ---ACTTGGTAAGATTAGCTT	20034824
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OY	4834	tgcattgtagctcttttccagagattctacagcctggagttaaagtcattgcacaaactctc	4893
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OY	5004	cctgaagagatgcgaatagccttaagaatttccaagagcttatcatatagtcagccctgtg	5063
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D	197812	AGAGTTTAACTCAGACTGTAGAGCCCTGGCCAAAGGCCAGTGGCCATCTCTAAACAA	1977535
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D	197632	TCATGCTGTAAGTGGTGAGCTTTTAATTAAGTAACTTAACGAGACTACCTATTACGCTATAT	1975737
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DB 194861 TAAAAAGACGAAGAAATGTGTGATTCAAGAGACTTGGATTTTAAACGACAGCTTGCTGAT 1948020

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RESULT	4
LOCUS	HS454G6
DEFINITION	Human DNA sequence from PAC 4546 on chromosome 1q24. Contains tripartite meshwork inducible glucocorticoid response protein, tRIP, myocollin, ESTs and STS.

ACCESSION 298750  
VERSION 298750.1 GI:2887277  
KEYWORDS 1q24; myocillin; TIGR.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eukarya; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 79376)  
Deadman, R.  
Direct Submission  
Submitted (27-Oct-1997) Chromosome 1 Project Group  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humque@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk  
On Feb 14, 1998 this sequence version replaced gi:2465060.  
IMPORTANT: This sequence is not the entire insert of clone 454G6.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we arrange for a small overlap between  
neighbouring submissions.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variations annotated may not be found in the sequence submission  
corresponding to the overlapping clone as we submit sequences with  
only a small overlap as described above.  
This sequence was generated from part of bacterial clone contigs of  
human chromosome 1, constructed by the Sanger Centre chromosome 1  
mapping group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1/  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The true left end of clone 454G6 is at 1 in this sequence. The true  
left end of clone 560B9 is at 79273.  
454G6 is from the library RPC13 constructed at the Roswell Park  
Cancer Institute by the group of Pletier de Jong.  
For further details see http://bacpac.med.buffalo.edu/  
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AA313383; match: AA163561 F02925 AA131540 W00634 R36066;  
match: AA313383 AA163561 N89173 AA174814 AA057059; match:  
AA329084 W47082 AA043955 AA341783 AA333681; match:  
AA046487 AA369741 H08313 AA186895 H32730; match: H08333  
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5216. 5345  
repeat\_region  
/note="Aluio repeat: matches 132. 1 of consensus;  
incomplete repeat"  
7759. 7907  
repeat\_region

repeat\_region  
/note="MIR repeat: matches 174. 1 of consensus"  
7933. 9328  
repeat\_region  
/note="TIGER1 repeat: matches 1. 1472 of consensus"  
9332. 9626  
repeat\_region  
/note="Alusg repeat: matches 1. 289 of consensus"  
9639. 10335  
repeat\_region  
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10343. 10642  
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10643. 10856  
repeat\_region  
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10949. 11384  
repeat\_region  
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/note="18 copies of 2 mer 83 & conserved"  
16856. 17286  
repeat\_region  
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17287. 17574  
repeat\_region  
/note="Alusg repeat: matches 15. 300 of consensus"  
18294. 18650  
repeat\_region  
/note="THE1B repeat: matches 358. 1 of consensus"  
18877. 19180  
repeat\_region  
/note="Alu repeat: matches 301. 2 of consensus"  
19767. 20013  
repeat\_region  
/note="LTR internal repeat: matches 5002. 4750 of  
consensus"  
20051. 20118  
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/note="LTR repeat: matches 539. 471 of consensus"  
20130. 20261  
repeat\_region  
/note="Alub repeat: matches 131. 1 of consensus;  
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20264. 20722  
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/note="LTR repeat: matches 482. 1 of consensus"  
20858. 21223  
repeat\_region  
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21216. 21302  
repeat\_region  
/note="LTR internal repeat: matches 4520. 4433 of  
consensus"  
21403. 21703  
repeat\_region  
/note="LTR internal repeat: matches 3887. 3580 of  
consensus"  
21978. 22357  
repeat\_region  
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consensus"  
22363. 22524  
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/note="LTR internal repeat: matches 2495. 2317 of  
consensus"  
22531. 22839  
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/note="Alusx repeat: matches 302. 1 of consensus"  
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misc\_feature  
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complement(23652. 24072)  
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24008. 24290  
repeat\_region  
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25895. 26364  
repeat\_region  
/note="LTR repeat: matches 2. 449 of consensus"  
26397. 26697  
repeat\_region  
/note="Alusg repeat: matches 1. 302 of consensus"  
26719. 27021  
repeat\_region  
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29037. 29334  
repeat\_region  
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30028. 30310  
repeat\_region  
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30402. 30539  
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/ncore="AluY repeat: matches 300, .1 of consensus"
repeat_region 32200..32301
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repeat_region 33283..33399
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repeat_region 33408..33667
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repeat_region 33956..34043
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repeat_region 34725..34904
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incomplete repeat"
repeat_region 34907..35207
/ncore="AluY repeat: matches 300, .1 of consensus"
repeat_region 35212..35344
/ncore="AluJb repeat: matches 133, .1 of consensus;
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repeat_region 36345..36842
/ncore="AluJo repeat: matches 299, .1 of consensus"
repeat_region 38190..38379
/ncore="MER3 repeat: matches 209, .13 of consensus"
repeat_region 38382..38682
/ncore="AluX repeat: matches 1, .302 of consensus"
repeat_region 38836..38968
/ncore="MIR2 repeat: matches 145, .2 of consensus"
repeat_region 38983..39279
/ncore="AluJb repeat: matches 3, .296 of consensus"
repeat_region 39418..39773
/ncore="HEI1A repeat: matches 354, .2 of consensus"
repeat_region 39775..40120
/ncore="HEI1B-INTERNAL repeat: matches 1580, .1234 of
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repeat_region 40757..41023
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Best Local Similarity 76.5%; Pred. No. 0;
Matches 5300; Conservative 0; Mismatches 970; Indels 654; Gaps 57;

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Db 11026 GGCCTGGGGCTCCCTGGCTTAACCCAGAGTAAATAAACAACCTCTGACTTAAGAAACCA 11085
QY 2219 tgcgtatcatatgattccagacatgtatagtaagggcattgtatgtaaggaacattgtga 2278
Db 11086 AGCTTACCCATGATTTTCAGCGCATGTGTATAAAGAAACA-----TGTGGA 11129
QY 2279 atctctgcttctgtctgttcaatctgtgacacacgggtgtctacagccctgtcacgtac 2338

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Dh	11190	CCCTGATTTGGCTTCATCATCAATCAACGACCCTTTCATG-TGAAATCTTAGTGTGAGCCC	11248
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Dh	11249	TTMAAAGGACAGAAATTGTGACACTCAGGAGACTCGAATTTTAAAGCGATACCTTGCCAA	11308
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Dh	11309	TCCTCCACAGCTGAATTAAGCC-CTTCCTTTCTTAACAATTGtGTCTGAGAGGTTTGTCTC	11367
Qy	2519	cgcgcatactcgtaacattctctgtgtctccctgaccgggaagcaagtgtaataacagatg	2578
Dh	11368	CGGCGTGTCATCTCATATTTCCTTGTTCCCTACCGGGAAAGAGAGACAAACCTGG	11427
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Db	12250	-----GACACACAGCATAGCGCGCTGGCAGAGCGAA	12280
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Oy	3931	tgaataaattacacg-ctgtttaaagaaagaatattgttaataagtcagaagaattag	3989
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Qy	6300	aaaacatcaacaggaagatcttctccttaaaattggagcttgtaacgtaaagactcaac	6359
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Qy	6840	acttgaataaaggatgaataaagaacccgttttagctccaaaaagagaaggaacccctcc	6899
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7111..7605
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7537..7559
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BASE COUNT 2607 a 1555 c 1646 g 1920 t
ORIGIN

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Query Match	12.7%	Score 3159.8	DB 11	Length 7728
Best Local Similarity	73.3%	Pred. No. 0		
Matches 5341; Conservative	0	Mismatches 497	Indels 1453	Gaps 43

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OY	2126	tagcccgccgcctaggaaccagacc-----gaaaccagccctg	2165
Db	1358	TAAACCAGGCGCTTAGGAACCAAGACCCGAAACCAAGAAACAGATCTGAAACCAAGGCGTGG	1417
OY	2166	gcctgcctgacctaagctcgtgagttaaaattcgacc-----cctgacctagcaactgtt	2220
Db	1418	GCCTCCCTGACCTAAGCCCTGGTAGTAAATAATCCACCCTCGACCTGACCTGGCAACTGTT	1477
OY	2221	gttacctatagttctcagacatctgatagtgaagggagattgtatgaagagacattgtgaaat	2280
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OY	2281	cctcgtctctgtctcttcttcaactgtagcaaccgcgtgtctacagccctctcaagtaacc	2340
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Db	1936	GCCTGCGCAGACCGCTGTTGTGGCAGGCCCCCTGGGAGATCAACGACGATGGCTGAACACC	1995
OY	2761	gggaagga-----ttggcaactggyagttccggaacataaaactgtgtaagctatgct	2813
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[illegible][illegible]

Db 59009 AAAATTATGCAAAAATGTTGTATATTTAAAGTAATAAGCCCTCGTAGTACTATT 59068  
Qy 4096 gaagaacagttctatgycagagtcgacaagaagaataatactcttggttaaaaga 4155  
Db 59069 GAAGAAACAGTTTATGTCAGCAGGTGTATAGGAAGTTAAATATCTTGGTTAAAGGA 59128  
Qy 4156 ttaagaagagccataagaatgtgatatctttacccatataaaggtt-aaaaaatctt 4214  
Db 59129 CTATAGAGGACATAGATGTGATTTTCTTACCTACATTTAAAGTTTAAAGAAATCTTT 59188  
Qy 4215 gttttgaagtttaagcaagttttaaaatgttaattgtaaaaaaaatctgtygttaa 4274  
Db 59189 GTTTTGAAGTTTAAAGCAAGTTTAAAGCGTTAATGT-AAAAGAAATTCGTGTGTAA 59247  
Qy 4275 ctaattgctaaagaataaaaggtatcatccaagtttctctgtaacgtgacattaaat 4334  
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Qy 4335 aaatgcaacaggttctctgtaagcaacacccgtctcttaacaataataaaggt 4394  
Db 59308 AAATGCAACAGTTTCTTAAAGCACAATCTCTCTTTAACAAAATTTTAAAGGT 59367  
Qy 4395 taagaagagtcgttaaaacttacctatggtcaaaactgaaaaaatggtataatgctc 4454  
Db 59368 TAAAAAGAGTCTATAAATCTTA-CTTATGATCAAAACATTAAATTTAGATTAATATGTC 59426  
Qy 4455 taagaagtttataaaaaatgaatttaacattataacacactaataaagaagtaatt 4514  
Db 59427 TACAAGGTTTATTTAAATTAAGTTTAACTTAATTAACACACTAATTAATAAGTAAT 59486  
Qy 4515 taagctatctggtlaaaaaacatacaagaagttatlaataataatgtygttagc 4574  
Db 59487 TAGCTTATCTAGTGTAAATCATACAAAGCAATGTTAATGTAAATGTTATTTGGC 59546  
Qy 4575 tttcttggtctaaacttaaaaaataggtcctaaagaacaatcttactagag 4634  
Db 59547 TTTCTTGGCTTAAAACTAATAAAATAGGTGTAAAGAAACATTATTTTAAAGAA 59606  
Qy 4635 gatcatgaagtttaagaagcttaaaacaaacttggcaattagaagaagatcccaagatgc 4694  
Db 59607 GATATATAAGTTTAAACTTAAACAACTTTTGACATTTAAGATGATACCAAGATGC 59666  
Qy 4695 aaatgacctggttgaatgtaataatcatcatctgcatataaacaagaagctgtgta 4754  
Db 59667 AAATGCCGTGTGAATGATCAATATTCATCTGCAGTTAAACAAAGAAATTTGTTA 59726  
Qy 4755 tgccttgycacatgycagagccagagccctcatggtcccccctccaataagtggtcctc 4814  
Db 59727 TGCCTTGTCACATGCGAGGCGCAGGCCCTGATGTCTCCCTCCACTAAGATGCTCTC 59786  
Qy 4815 cagtcacccacagcggtggtgctcatgtagctctttccagagattctaagctgtagtaa 4874  
Db 59787 CAGTCGGCCAGCGCTGGCTCATGTAGTGTGTTTCCAGATTTCTAAGCTGGATTAA 59846  
Qy 4875 taatcatgccaasactctctgctat-----ccctgtgggtcagccccc 4918  
Db 59847 TAACTCATGCCAGGCTCTCTCTGTCTATATCCCAAGTCTGTGATACCTGGGTGAGCCCC 59966  
Qy 4919 cgaagggccatccagcctcgtctcccaacactaagttcacttc-atgctctcacacag 4977  
Db 59907 TGAAGGCCATCCACCTCCGCTCCCAACACTAAGTTCACTTGCTGTCTCCAGACAG 59966  
Qy 4978 agaggaagaactaagatctccttggaagactgaagtgatgcaatgagcttaagaatttcaa 5037  
Db 59967 GGAGGAAACTTAGATCTCTTGAGAGACCTGAAGGATCGATGACCTTAAGAAATTTTCAA 60026  
Qy 5038 gaggttaaatcaagtcagccctgtgtlcatccccaagcgagtgtygtgttatgtggt 5097  
Db 60027 GAGCTTATCAATCAATGCTAGCCATTGTTATCCGACAGCAGATGTYGTGTATGTGCT 60086  
Qy 5098 ggaacttaactgagcactctgccaataactggaagtggcacttaacttaagtcaggtg 5157  
Db 60087 GGACCTTTACGGGCGACCTGCCGATTAACGGAAGTGACACTTAATCTTAAGTCCAAATTG 60146

Qy 5158 gctatcccttcacocctggtcatcatcaacaagagggaggaataataagatcgtgtaa 5217  
Db 60147 GCTATCCCTTTCACCCCTGGCATTTTCATCAACGAGAGGAAAAAATAAGACATTGTAA 60206  
Qy 5218 gcgagagaagccccccttaaggtcttctgactctcaagctccatctagaagcaatgtagt 5277  
Db 60207 GTGAGAGAAAG-CCCTTATAGTCTTTGACTCTCTCTCATTTAGACGCGAGTTGGAGT 60265  
Qy 5278 cccacaggaatcacagaatcaatgaagcttgaatcaaatagctacaataattagctc 5337  
Db 60266 CCCACGAGGAATA-CAGATCATTTTAAAGCTTGAATCAATTAAGCTACGATTTAATTC 60324  
Qy 5338 aatatttagtgatgta-tgttaataaaatgtaattagataaattatctatctaacaa 5396  
Db 60335 AATATTATAGTAGTGACAGTTAATAAATAAATTAATTAATTAATCTATTTACAA 60384  
Qy 5397 acaacagaacaagcttcttcaatgagttgaagaaaaaactcaggtcggcccaagccctgg 5456  
Db 60385 CCAACAGCAGCAGGCTTTTCATGAGTTAAAGAAAACTCAGTCCGCGCCCGCTGG 60444  
Qy 5457 gctactgacctgagcaagatgacacactctatggtccaaaaaaatgtaaaaaaagg 5516  
Db 60445 GCCACCTGACCTGACAAAATTTTACACTATGTGTCAAAAA----- 60490  
Qy 5517 gccatctatccaattctaaagtttaagactaaacaaggtcttactcatagcaagya 5576  
Db 60490 ----- 60490  
Qy 5577 taatgtaaatcccaacttiacaagtttcaacaagaataagtttgctaaagttaca 5636  
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Qy 5637 gtytaacatgataatagtaactcttaactctgtyggccttagacagttagtcacagat 5696  
Db 60490 ----- 60490  
Qy 5697 ataagaagttcacttaaaaaaaatgaatggttatcttcaaaaaaaat 5756  
Db 60490 -----AAAAAANAAT 60502  
Qy 5757 ggcagttgagtttbaaccagactgtaggtctctgycgaagccagtggtctatctc 5816  
Db 60503 GGCAGTTGAGTCTTAACCCAGACTGTAGGCTCTGCGCAAGCCAGCGCTATCTCTC 60562  
Qy 5817 aaacaactaagatggtgttccaaagctggtcccatatctaagggccctcgcaagcaac 5876  
Db 60563 AAAAC-ACTAAGAGGGGTTTCCAAAGCGTGGCCCATGTATAAGTCCGTGGCAGCAAT 60621  
Qy 5877 ggcctgttagcacagaagcagataagctaacctcttaggcaaaaactaacaataagtc 5936  
Db 60622 GACCTGTTAGCACAGAGAGAGATAGCTAATCTTAGGCAAAAACCTAAGT----- 60675  
Qy 5937 ccccccaltgctgtgacttaatcagttacaaagacatcatatagcttaatgtaagta 5996  
Db 60675 CCCCCATGCTGTGATCTTAATAATTAACCAAGACATCATAGCTATGATGCTA 60734  
Qy 5997 gactaactagatcacaaagctgtctgtgtaaaatccccaataacatctgaagttgca 6056  
Db 60735 GACTTAACATGATACCAAGCTTGCTGTGTGAATAATCCCTGATTAACCTCCAGATTGCA 60794  
Qy 6057 aacccctaaaccccgccaccttgcctcgtatagaagagccaggttaaaataactgtg 6116  
Db 60795 ACACCTTAACCCAGCCCTTACTCTCGTATAGAGAGCCAGTTGAATATACATATCTG 60854  
Qy 6117 tagaagttgtagtcaattatctlaagtggtgccaactccaaacactccttaaacat 6176  
Db 60855 TAGAGCTATTGACTCAATTTATCTAOTGTGGTCCAACTCCAAAGCATCTTAACAT 60914  
Qy 6177 caatnaactggagctgtacgtgagtgaggaagccttcaaccaactctgcaaaagtgatc 6236  
Db 60915 CAGTAGACTGGAGCTGTAGCTGATGGAGACACTTCCCAACCCCTGCAAAATGATTC 60974



QY	6237	aga-----aaaagccctgtccagttacaccccggaagctgacgtgtccacgcgcgcg	6288
Db	60975	TTGAAGAAGCAGCAACCGGTGGTCCAGTACACCCGGAAGCTGACGTGCATCTATGGC	61033
QY	6289	cgaagcatgagaaaactcaacacggagactcatttcccttaaaattggaactgtacagta	6348
Db	61033	CGAAGCATGAGAAACTCATCCGGGACATTTTCCCTTAAATTGGACTTGCACAGTA	61099
QY	6349	aggacttcaactgacaccttccctcagactgagaactgtgtcccgatataatacacaagtact	6408
Db	61095	AGGACTTCAACTGACCTTCTCCTCAGACTGAGACTGTTCACAGTATATACATCAAGTCAC	61155
QY	6409	ggagttaggcacaaagattgtctacagtccattatttcattcgtgtattatagaagtacagag	6468
Db	61155	GGGATAGGTAAAGATTTCTCAGCCCATTAACITTTATGGTATTTATAGTATACCGGG	61214
QY	6469	actctcaaaagaacctgtgttctgataatgtctattctataccaagtatgtatggccgaagaat	6528
Db	61215	ACTCTAAAGAAACTGTGTTGCATATGCTATTTCTTCCAGGTATGTATGACCGA-----	61266
QY	6529	aaccacactgattgtgttatgacccattttaagccctccaatgatacacagtttttaaa	6588
Db	61269	-----	61266
QY	6589	taattaaagactgtgtcccttcttctagtgtacacaaagtaagtatatgtctaaagacaga	6648
Db	61269	-----	61266
QY	6649	aagaggaatccccaagcaltgtacaactaaatttaagtctgtgcacatacatagca	6708
Db	61269	-----	61266
QY	6709	tccgcatagaataagatgcggttctttaactgtaaaaaaaagttcacacagcagsgaa	6768
Db	61269	-----	61266
QY	6769	ataagtatatcgcgcacgagattaagctcatgtgcgaatgtgtgttaattactgttctgtg	6828
Db	61269	-----	61266
QY	6829	tcatctaggtacttagaaaaagatgaaaaagaccctgttagctccaaaaagsgaag	6888
Db	61269	-----	61266
QY	6889	gcagccctcctgtacgagtggaagctgcacaccctgaaatagtataacaacatccct	6948
Db	61269	-----	61266
QY	6949	taaacccaagttagaaaaaaagaagtaacgctatctctgtggtcgatataaaaagacta	7008
Db	61269	-----	61266
QY	7009	gattcctagtaaatatccttagtaaaagsgaggttcgttaactctctccgaaccagta	7068
Db	61269	-----	61266
QY	7069	tttcgacttctatgattaactaaatgtgcagtaacagagaatccagaaaaaccaga	7128
Db	61269	-----	61266
QY	7129	aattgttttttcgaattgacgagcatgtacgccagtcctctaattgtcaaccctaatctac	7188
Db	61269	-----GTCCTAATATGTTAT	61283
QY	7189	gtttgtgagaacctgtaaatagaagatcaatgg-cataagaagcccgagaattagtcct	7247
Db	61284	GTTGTGGAGGACTGTATACAGAGATCATATGGCCATTAAGAAACCTCGAAGATTAGAGCCT	61344
QY	7248	aaagaccccgcttcctgtatgaattcccgcgcccaaaaagataccctgtatcatcttctaggt	7307
Db	61344	ACAGACCCAGTTCCTGATATGAATTTCCAGGCCCTTAAAGAAATCACCCCTGATCATTTCTAGGTT	61400
QY	7308	ctaaaagctcaattatttagacanaattgtcatagctgtgaaaaaaggaagaatcatctcat	7367

D	b	61404	CTAAAGTTTCAATTATTGGACAAATTTTCCAAAGCTAGAAAAAGCAAAATTTCACTCAT	61465
Q	y	7368	ccctgtagtgacttagtctccttaggacaaaactgtataatggtaccacaaaacagtt	7427
D	b	61464	TCTGTAGATGACTTAGTTGCTTAGGACAAAAACGTGTATATAGTACCAAAAAACAGTT	61522
Q	y	7428	acatggtgagttcaaacacacagataaaatccatctagtaaatcttccaaagtgcag	7487
D	b	61524	ACGTGGTGGAGTTCAAAACACACAGATTAATAATTCATTCAGTAGATTTCCAAAGTTGCAG	61583
Q	y	7488	accgctttagcccccacccaagaattccacgsgactgagagccccccacacagctacag	7547
D	b	61584	ACCATTTAAGCCCCACCCCAAAATCCACCGGAGCTGAC-GGCCCCACATAGCTATACAG	61642
Q	y	7548	gatacgtgacatagaacctacgctgaagctgctgcacagtgagcagagttgtgtat	7607
D	b	61643	GGTATGTGACACTAGAACCTAGCGTAAGCTGGCTGACACAGTGGTCAAGTAGTTGATTAT	61702
Q	y	7608	tgggacatataacacatcttctcctactgcccatacaataagcgaaectccgtggtt	7667
D	b	61703	TGGCACTATTAAACATCTTTCTCTTACTACCCATAAAAAGCGCAAACTCTGGGCTT	61765
Q	y	7668	ccctctctatgtttcccgsgaaagcgaaacatacagtagtaatttaaaagatgata	7727
D	b	61765	CCCTGCTATGGTTCTCTGAAAAAGAAAGCATAGCTATAAAAAATTCAAAATATATA	61822
Q	y	7728	atgaccacacctaa-aaattatatacaatactatagcgctgcacttagacacaagatgccc	7786
D	b	61823	ATAGCCCCCTAAGCAAAATCATCATATATATATATATAGGCGCTGTACTTAGGCAAGACAGCTC	61882
Q	y	7787	atgggtatacagaccccacttaacatgctcaactgcaatcgaatacaggtgtgcaagctgttt	7846
D	b	61883	ATGGGATTCACGACGCCCATTTTACATGCTCACTCACTGAACATATAGTTGTCAGCGCTTCT	61942
Q	y	7847	agaaatcatcacataataaacacagfcaaacgcttgactatctcggcccgacaagaactca	7906
D	b	61943	AAAAATCATCATTAATAAANACTGTCAAGCTTGACTATTCTGGCCCGCAAGAACTCA	62002
Q	y	7907	gataagaaatgctatctatcatcaaatagatltgctctgcactact-ctagcagctgaaag	7965
D	b	62003	GATTAAGAAATGCTATCTATCAATAATAGATTTGGCTCGCACTACTTGCTAGCAGCTGAAG	62065
Q	y	7966	agaaggtctataa-aaattaaecttaactaatctgctctcaacatagataatcaaaagca	8024
D	b	62063	AAAGGTCTATAAGAAATTTAACTTACTAGTCTGTCTACCAATAGATAATCAAAAGCA	62122
Q	y	8025	agtagttaagacgtagttaaagacatagtttaaaacatgacaaaactgscacatgccc	8084
D	b	62123	A-----GTAAGTAAAGACATTAATTAAATAATAGCAAAACGTGCACATGTGCC	62170
Q	y	8085	cgtaagagtgtagcaggaatctgcaccctgaagcccatgtttagaaggtgtgtccacagcat	8144
D	b	62171	TGTACAGATGTAACATGAGTTGTGACCCGTGAACCAATGTTAAGAGTGTGCCAGCACT	62233
Q	y	8145	aggaggaattaaactcttat-atagaggtataatagtaataagaacactgcttactgct	8203
D	b	62231	AAGAAATTTTAAACCTTATATATATAGAGTTTATATAGTAATAGCAACCTGCTTACTGCT	62290
Q	y	8204	cccttgctgtcgcctgttactcttccaatgtataaaagctcatgtcactcttagttca	8263
D	b	62291	CCCTGTGTGTGCTACCTGTACTCTTCAATGATGATAAAAACCTTCATCACTTGTGATTTA	62356
Q	y	8264	ccaaaatgcttaacacaaagtgtactataatgaactcaactcaatctatgacaaagag	8323
D	b	62351	CCAAAATGCTTAGACACAGATGTACTATATGTAGATCACTTCAATCTATTGCCAAGAA	62411
Q	y	8324	cataagtggtcaaaaaataagtgtagaactcccaactataaaaaagtgtagtctcaaaag	8383
D	b	62411	TGTATGTAGCAAAATATAGAGTGAAGACTCCAACTAATATAAAGTGAAGCTCTCAAGG	62470
Q	y	8384	gggaaatgaggaagagagagacccctctcatatgttttataatgttttatactcagaa	8443



Db	62471	GGGAATAGAGGACAGAGACACCTCTC-----ACGTTCTTTTATACGTAGAAA	62520
QY	8444	aggacagagaagcgaactaaagcaggtagccggcgactaagaacagac-----	8496
Db	62521	AGGAAGAAGAAAGAGAAAAAGCAGGTAGCCCGACGACCTAGAAACCAAGACTGMAAC	62580
QY	8486	-----ccgaaccacggcctggcgccctgacgctcaagcctgtagtaaaatt	8543
Db	62581	AAGGAACAGATCTTAACACCAAGCCTGGGCGCTGCGCTGACCTTAAGCCTGGTAAATAATT	62640
QY	8544	cgaccctcgaccctgaacactggtgtatcatatagattccacacatgtatgaagacat	8603
Db	62641	CCACCCTGACCTACACACTGTTGTTATCTATAGATTCCAGACTTGTATGGAAGAGACT	62700
QY	8604	tgtgaatctctcgltctgttctgttlltaactggtgacacacagtgctcaagccctgtca	8663
Db	62701	TGTGAACCTCCCGCTTCTATTCTGTGTCACTGTGCATCGGTGCTCACAGGCCG-GTCA	62759
QY	8664	cgtaacccctcgacttaccatcgtatcgtaacgacctcatatgaagaccccttagagttgt	8723
Db	62760	CATACCCCTTGCTTGGCTTCATCAATCACAGACCTCTCATGTGGACCCCTTAGAGTTGT	62819
QY	8724	gagcccttaaaaggcagaagttgagcacacttgacagagctcggatlttgaagcgtacgc	8783
Db	62820	TAGCTCTTAAAGGACAGAAAGTTGAGACACCTGAGAGAGCTCGATTTTAAAGCGCTAAGC	62879
QY	8784	tgcgcattctcccaagctaatgaagcacactccctcaactatctcggtgtcgaaggggttt	8843
Db	62880	TGCTCATCTCTCCACACTATTTAAACCACTCCCTTCACTATCTCGGTGTCTGAGGGGTTT	62939
QY	8844	tgtctgcagctgtctcgtctacacgtgtaagcta	8876
Db	62940	TGCTGTGCTCATCTCTGCTACACAGTAACTTA	62972
RESULT	7		
LOCUS	HSJDJ636H5	116679 bp	DNA
DEFINITION	Homo sapiens chromosome 1 clone RP4-636H5, *** SEQUENCING IN		
ACCESSION	AL21602		
VERSION	AL21602.1	GI:5002330	
KEYWORDS	HTG; HTGS_PHASE1.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 116679)		
JOURNAL	Pavitt,R.		
COMMENT	Direct Submission Submitted (29-SEP-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hinxton@sanger.ac.uk Important: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dj636H5 Contig_ID: 00009 acc- length: 10030 bp Unfinished: dj636H5 Contig_ID: 00013 acc- length: 3796 bp Unfinished: dj636H5 Contig_ID: 00014 acc- length: 1463 bp Unfinished: dj636H5 Contig_ID: 00018 acc- length: 3590 bp Unfinished: dj636H5 Contig_ID: 00035 acc- length: 3490 bp Unfinished: dj636H5 Contig_ID: 00063 acc- length: 5077 bp Unfinished: dj636H5 Contig_ID: 00091 acc- length: 1090 bp Unfinished: dj636H5 Contig_ID: 00114 acc- length: 5558 bp Unfinished: dj636H5 Contig_ID: 00132 acc- length: 1293 bp Unfinished: dj636H5 Contig_ID: 00164 acc- length: 3396 bp Unfinished: dj636H5 Contig_ID: 00174 acc- length: 2086 bp Unfinished: dj636H5 Contig_ID: 00175 acc- length: 4631 bp Unfinished: dj636H5 Contig_ID: 00227 acc- length: 1546 bp Unfinished: dj636H5 Contig_ID: 00239 acc- length: 3784 bp		

QY	2626	gcctggagatccaaacagccagagtgacgcgagctctcgagacgtctccctggatggacat	2685
QY	2566	gattacagagatgctcgagcagcgtccttgagcggctttagcctctgcgccttggaaacacc	2625
Db	54111	GACTGAC-----GGCCGGCTTAACTGCGCCCTGTGAGAGGTGCC	54149
QY	2506	gggggtttgtctcggggtcattccctgtataatttcttggttcccttgaacgggaaagagt	2565
Db	54051	AGGTTTGTGTCGCGCGCTGTCTCTCAATTTCTGTGGTTCCTTACCGGGAGAGGAGGT	54110
QY	2386	gggttggtgagcccttaaaaggagcaaggttagatcaagagagctcgatatttgaagc	2445
Db	53931	GAGTTGTGAGCCCTTAAAGGAGACAGGAATTTCTCACTCGGGAGTTGGAATTTAAAGC	53990
QY	2446	gatacgtctccgattctcccaagctattaaagcaactcccttcaactatctcgtgtcgtg	2505
Db	53991	AGTAGGTTCCGATGCTGCCAGATGATGAATTAAGCCCTTCTCTTACAACTCGGTGCTGAG	54050
QY	2326	ccgttcacgtaccccttggtcttactcaatcgtacacgaccctctcatgcygagccccctta	2385
Db	53872	CCTGTACGTAAGCTTCTGCTGCTCAAAATCAATACAGACCTTTGATG-TGAATTCCTTA	53930
QY	2266	aggaatattgaaatcctcgttctggttctgttctttagcttgacacacgggtgtctcaagcc	2325
Db	53812	AATAACACTGTGAACCTCCTGCTGCTGCTTCTTCTTCTGTGACACCGGTGCATGACGC	53871
QY	2206	gacctagcaactgtgttatctatagatctcagacatgtatgtgaaaggcatgtatgga	2265
Db	53767	AACCTTAAACCGAATGTTTATGATGATTCACAGA-----CATTTGATATA	53811
QY	2146	agaccggaacacaggcctcgtgacctccttactaaagctcgtgtagttaaattcgaacct	2205
Db	53707	AGGCCGGAACACAGGCCCTGCGCTTGTCTTACTTAACCGAGTAGTTAAATCAACTGCT	53766
QY	2086	tattactcagaagaagaagaagtgaattaaagtcagatgcccgcgccttagaac	2145
Db	53647	TCTTTTAAAGAAAAAAGAAAAAAGACAGAGTAATTAACCAAGAGACAGCGCCGCGCC	53706
QY	11.6%	Score 2884.2; DB 32; Length 116679;	
Query Match	Best Local Similarity	66.9%; Pred. No. 0;	
Matches 5667; Conservative	0; Mismatches 1568; Indels 1242; Gaps	60;	

Db	54150	ttgaggggagactccagacacactttagtgagagcc-gatccaaanaagatgctcccggttaggcga	542083
QY	2686	ttgcccgcggtgggaacacctccgcgaagcagtgctgtgcagggccccgcgtggaagatcaaca	2745
Db	54209	ttggccccaatggaaacccgctgcgcagagcagcatgttagcaggcccccacacagagatattaa	542688
QY	2746	gagtgagctgaacacccggagaaggaattggaacttgagctgcgcgacataaactgaacttgtaa	2805
Db	54265	cagtgagcttaaacaccaggaaggaactggcactttggagctccggacatcttaaaacttggtaa	543282
QY	2806	gactagctcttggaaacttg-cccactccactttgagtgaagcagatgagctgtacaccag	2864
Db	54329	gactagctcttggaaactttcccccactccacttgagtggaagacatgagctgacatccacag	543888
QY	2865	gagtgagcttaacagcagacttggttggcttggacttggttgaataacttgacaggaact	2924
Db	54389	gggggctctccattggcacttttg-----	544122
QY	2925	ggtcttggaaacttgcaccatccatccactccacttattggaagcaatgacgtcatct	2984
Db	54412	-----	544122
QY	2985	gattacccaagtgctgctgtccgcgacacttggttcttggcttggacttgacatagatt	3044
Db	54412	-----ttcgggttttaacttgacttgaatt	544388
QY	3045	gcttataacttggttggcttggcttgaacctgcgcttgagatctcgaataacttgaatttgct	3104
Db	54437	gctggaacttggcttggcttggcttggacttgccttggaatttttggagctcggaattttgaa	544566
QY	3105	tt--tgatttggctttagtgaacatgcgaagaatgctgctgacccctttaccgcctc	3161
Db	54497	tttcggatttttgggttggtgaataaaacgtaaaagtgatgtgccttttttaactgcttc	545566
QY	3162	tttgttttggtg--gtgcatgctggtgtagagtggtgttggctcgcgaagaacatg--	3219
Db	54557	tttgtcttggctgagctgctgctgagtgatgagcatggtatttttgatcaaaaaaaaac	546166
QY	3219	-----gtcagcgacaataagcccaacccactagaaacatgttgaa----aattcaa	3269
Db	54617	agcatggggtcagagcaaatatgaagccacccacatagaaacatgtttaaanaagaaatttcaa	546767
QY	3270	gaagaagatttaaggagagattacggtgttactatgtacatacagaataaacttaagaacttg	3329
Db	54677	gagagaaatttaaggagagattatagcgtttactgtggcaccaggaataaacttaaaactttgg	547366
QY	3330	taaaatagaactgccaacatagagtgagtggttgcacatcagaagaagacttaagcaggtc	3389
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RESULT	8
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DEFINITION	Homo sapiens chromosome 1 clone RP4-603114 map p31.3-33, ***
SEQUENCE	SEQUENCING IN PROGRESS ***, In unordered pieces.
ACCESSION	AL122001
VERSION	AL122001.6 GI:6523744
KEYWORDS	HTG; HTGS-PHASE1.
SOURCE	human.
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 162921)

TITLE Direct Submission  
JOURNAL Submitted (03-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire  
CE10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On Dec 3, 1999 this sequence version replaced g1:6165528.

IMPORTANT: this sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig\_ID: 00021 Length: 16812bp

Contig_ID: 00165	Length: 8819bp
Contig_ID: 00883	Length: 1107bp
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Contig_ID: 02332	Length: 5886bp
Contig_ID: 02381	Length: 1435bp
Contig_ID: 02392	Length: 1014bp
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Contig_ID: 02612	Length: 1567bp
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Contig_ID: 02654	Length: 1435bp
Contig_ID: 02690	Length: 6013bp.

\* NOTE: This is a 'working draft' sequence.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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/map="p31.3-33"
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BASE COUNT      39921 a 35776 c 34511 g 37110 t 15203 others
ORIGIN

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Query Match	11.5%;	Score 2879.4;	DB 33;	Length 162921;
Best Local Similarity	66.98;	Pred. No. 0;		
Matches 5657; Conservative	0;	Mismatches 1568;	Indels 1242;	Gaps 60

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OY	2146	agaccggaacaccagagccttggccttcgcttaccctaaagctcgtgagttaaatctcgaccct	2205
Db	51831	AGGCCGAACACAGGCGCCCGGCTGCGCTGACCTAAACCAAGTAGTTAAAAATCAACTCAT	517726
OY	2206	gacctagcaactgtgttatctctatagatctcagacatgtatgtgaagggcatgtatga	2265
Db	51771	AACCTAAAAACCGAGTGTATTCATGATTTCCAGA-----CATGTGTAGA	517227
OY	2266	aggaaatgttgaatctctcgtctgttctgttcttcaactgttgaccccggtgtctaaagcc	2325
Db	51726	AAACACAGTGTGAACCTCCCTGCCCTGTGTTGTTCTCTGTGAGCACGGGTGATGAGCC	516678
OY	2326	cctgtcacgtacccctcgtgcttacttcaatcgtatcaagaccctctcatgtggaacccctta	2385
Db	51666	CCTGTACGTACTCCTTCTGCTTGTGCTCAATCAATCAGACCTTTCTATG-TGAATCCTTA	516089
OY	2386	gaattgtgagcccttaaaaggagagaaatltgacatcagacagagctcggatltttgagac	2445
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OY	2506	ggagtttgtctgcgggctcatctcgtctaattcttgttcccttgacccgggaagcaagt	2565
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OY	2566	gataacagatgtctgaggcagctcctctgaaggcgcttaagccttcgacctgttgaaatccc	2625
Db	51427	GACTGAC-----GGCGGCTTAACCTGCCCTGTGAGGCGTCCC	513890
OY	2626	tgtctggggaatccaaccagagatgacgagatccttgaagctctctcgttgaagcat	2685
Db	51388	TGTGGGGGACTCCAGACACTTGAGTGAAGCGC-GATCCAAGAGTGTGCCGGGTAGCGAA	513330
OY	2686	ttgcccccggttggacaacctcgcgcagagcagtggttgtgcagggcccccggttgaagataaca	2745
Db	51339	TTGCCCAATGGAAAGCGCGCGCAGAGCGAGATGTAACAGGGCCCCACAGAGATTAAACA	512701
OY	2746	gaattgcgaaacacccgggaagaatttggacatttggatcgcggaacaactaaacttgtaa	2805
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OY	2806	gactagctcttggaaattg-cccactccaatttgaattgaagaatggtcgtatcaaccagc	2864
Db	51209	GACTAGTCTTTTGAAGTTCGCCACATCCATCTGAGTGAAGTGAAGATGGCGTGAATCACCAG	511503
OY	2865	gcgtgcctttatcaggaacttggtttggatttggacttggatttgaacttgaacgaagact	2924
Db	51149	GGGGGTCTGCATTTGCCACTTTTG-----	511265
OY	2925	ggtcttggaaacttgcccaactccatcccaactccatcttgaattgaagaagcatgacctgatct	2984
OY	51126	-----	511266
OY	2985	gatacccaacggtgtgcctgttcgcggaatttggatttggatttlttgaacttgatagatt	3044

[illegible]

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QY 3959 agaatattgttaataagtcagaagttagagacatgtaagaattatctgcgaagtca 4018
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QY 5558 tcttaccatagcaaaagatattgaataatcccaacttaacaaggtttcaacaaagtaa 5617
Db 48061 ----- 48061
QY 5618 agtttcaaaagttaacagtgtaacatgtatataagtaacttcaatctgtgacctta 5677
Db 48061 ----- 48061
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OY	5858	taagggccctggcagcaacgcccgtttaaccaagaagcagataagctaactcttaggc	5917
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OY	6503	tatccaaggtatgtgctcctaggaagaataaccaacctgtatgtgtttatgaaccattttag	6562
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OY	6563	cctccaatgatacaggttttttaaaataaataaaggaactgtctccttcttaagtgacaca	6622
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OY	6623	agtaagaataatgtctaaagcagaagaagaaggatctcccaagcatgttaacactaaattt	6682
Db	47190	AGTAAAGTATGTGCTAGGACCAAGAAAGAGGGGCTCTCAACCATATTAACCTTAATATT	4713
OY	6683	aatgctgtgccaatcataatagcaatcgccataagaataaggttcggttctttaaactg	6742
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OY	6743	aaaaaaaagtltacacagcaggaataagtaatactctccacgaattaaactcatgtgc	6802

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QY	3603	-----aga	3605
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Waterston,R.H.  
TITLE The sequence of Homo sapiens clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 163738)  
AUTHORS Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (24-AUG-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
COMMENT  
On Oct 15, 1999 this sequence version replaced g1:5762562.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 19420: contig of 19420 bp in length  
\* 19421 19438: gap of unknown length

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OY	3189	agagtggtgttctgtctcgaaagaacatggtgtcaggtcacaaataagccacccctctga	3248
OY	3189	agagtggtgttctgtctcgaaagaacatggtgtcaggtcacaaataagccacccctctga	3248
Db	17700	AGCTTAGTGTGTTGCTGTGAAMACATAGGCGACGACAAATAAGACCCACCCCTAGG	17759
OY	3249	aacttgctgaaanaa--ttcaagaagaagatttaagggagattcaggtgttactatga	3306
Db	17760	AACCTATTGTTAAAAAATTTTCAAGAAAGATTTAAAGAGATTACGGTGTCTGTGACA	17819
OY	3307	ctagaanaaacttagaactctgtgtlaaatalagactgtgccacattagaggtggttgcca	3366
Db	17820	CTAGGAAAACCTAGAACTTGTGTGAATATAGACTGCCAGCATATAGAGGTGGTGCCA	17879
OY	3367	tcagaagaagacgtctgac---aggtccctgtttccaatgtatggtcacaaagtactgt	3422
Db	17880	TCAGAAAGGAAGCTTGACAGAGTAGTGCTCCCTTTTCAAGGATATACACAAAGTAACTCG	17939
OY	3423	taagccaaggtccacagaccagttctctagtagacaattacagctgtgttagaccc	3482
Db	17940	TAAGCCAAGGCGCCAGACCACTTCCGTACATATACAGTTACACTGTTTAAACCA	17999
OY	3483	cttcgccccccagtagttaaagagagagaagaagagaaacagagcaaaagga	3542
Db	18000	CTTCCCGGCCCC-----CTAACAGATGTTAAGAGAA	18030
OY	3543	agtcaaaagagagagagagagagagagagacagaagaatcaaagagagaagaaaaatag	3602
Db	18031	CAGCGCATTAACGGCTGTGCAAGGCAAGGAAAGAAACAGCAAGCAAGAAACCA-----	18084
OY	3603	agagaataatccagtagttaaagaanaaatagttaccctcttcccttaagaagcaag	3662
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OY	3723	ataccacttgtgtgttagtgtlaaacaagggcgatcccgaaagcactgaagccctccat	3782
Db	18188	AAAGTTAACAGTATACGATATCATGTAATCTTAATCTTGCGCTTAGACAGCTTAGT	18247
OY	3783	caaaaatccctaacccagtaaccagcgatgccccagatgcatactctgtagcagag	3842
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OY	3843	ctgcttctctaacaggaaaaaaataaaagaagcgtgtggaagggcaaaattatgttaa	3902
Db	18275	-----AAAAAAGGGGTGAGGACAGATTATGTAG	18306
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OY	4137	tactcttgtgaaagaagttagaaggggcaataagaatgtgattttactacattaa	4196
Db	18547	TATACCTTTAGTAAAAAGTTTAAAGGAGCATAAGATGTGATTTTACTTAATTAA	18606
OY	4197	aaggtlaaaaaaatattgttlttgaaaglttaagcaaglttlaaaagttaattgtlaaa	4256
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QY	4317	gaacttgacattaaagttaaanaatgcaacaggtttctctgaaagccacacctgtcttta	4376
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Db	18786	ACAAAAATATATAAGGTTAAAAAGAGCTATATAAATCTTACCTTATGGTCAAACTATA	18844
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QY	4497	taattaaaggtaaaaattagcttctctgtgtataaaaacatacaagaagtattataa	4556
Db	18903	TAAATATAAGGTAAATTTAGCTTATCTGTATATAAGTACATCAAGAAAGCATTTATTA	18966
QY	4557	tataaaatgtgtttagcttctctctgtgtctataaaactaaataaaataggtccataa	4616
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QY	4617	acattcaatttactagagatcatagaaagttaaagaacttaaaaacaaacttggcaat	4676
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QY	4677	gacagcatcccaagatgcaaatgacctgtgttgaaatgagatcaaatatccatctgcac	4736
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QY	4797	tccactaaagtgtctctccagtcaccaacagcgltgggctgtcatgtagtctttccaga	4856
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QY	4907	tgggtcagagcccccaggggagtcacacagccctcggtctcccaacataagttcacctat	4966
Db	19323	CGGGTCTGCCCTGAGGGCATCCACAGTCTGTCTCCCAACATAAGTTCACCTTCTTGT	19382
QY	4967	tctcaaccaagagaaacttagaattcctctggagacctggaagtatgacaatgaacta	5026
Db	19383	TCTCATGCAAGAGAGAGAGACTTAGCATTTCTTGAGACCTGAAAGSATTGCAGTGA	19442
QY	5027	agaatttcaagagcttatcaatcagtcagccctgtgtcatccccaagcggagtgtggt	5086
Db	19443	ACAATTTTCAAGAGCTTATCATCATGATCACCCCTTGTTCAACCCCTCAGTGAAGTGT	19502
QY	5087	ggtaattgtgtgagaccttaccgtgggagacctgtccgaataactcgtggagtgcattact	5146
Db	19503	GATATTGTGTGTGACTTTACTTACGTGGGACACTCTGTGAATATCATAGATGGCACTT	19562
QY	5147	tatgcagagtgtgctatcccttccaccctgtgaattcatatacaaaagaggt-aggaa	5205
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QY	5206	agacatcgtlaaagcgagaaagcccccataagttcattgacttgcactccacgtccatt	5265
Db	19623	AGACATCATATAAGCGAGAGAG-CCCTTATATAGCTTTCACACTCTCGCATATTTAGA	19682
QY	5266	cgcgaattgaggtccccaaggggaataaccagatcaatttaaagcttgaatccaatagct	5325
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QY	5326	aaaatttaagtcataatttttagtggtgtg-tgttaataaaaatgtcaaatatagataa	5384



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OY	6873	-----	6673
Db	21769	AGAGCCTCCACACTCCTCTCCACCCGAATGGTTAGACTCTATATTAATAAACAA	21828
OY	6873	-----	6715
Db	21829	GGCTTTTGGAAAAAATAAATAATTTGACACTGTGGCTGCTACGATATGTAAGAGCAT	21888
OY	6716	agaataagaatcggtctttaa---ctgaaaaaataaagtacacacagagaata	6771
Db	21889	AGAAATMAATGGGGTCTCTAATATCACACACACAAAAAAGTTACACAGTAAAAATA	21948
OY	6772	agtaatctgcacgaattaaagctcatctgcaaatgctgtaattaccgtctgtgca	6831
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Db	22008	TCATG---ACTTAGAAAAAGATGAAAAAGATCC--TTAGCTGCAAAAAAAGAGAGCA	22062
OY	6892	gccccctctgtacgagtggaagctgcaacccctgaaattgtaattcaaatcccttaa	6951
Db	22063	GCCCTCCTGCATGAATAGAGGCTCCAAACCCCTTAATAATTATTAATTCAAATCCCTTAA	22122
OY	6952	acccaagtagaaaaaaagaagtagacglatctctgcygctgataaaaaagagtagat	7011
Db	22123	ACCCAAAGGTAG-AAAAAAGAGAACACATATCTCTAGCGCATCAATTAAGAAAAAGCTAAGT	22181
OY	7012	cctagaatgaataacctgtagtaaaagaagaggtctgtaactctctccggaaccgatttt	7071
Db	22182	CCTAGCATTAATCATCTTAATAAAGAGAGGTTCAAGATGCTCTCCAGAACCAATATTT	22241
OY	7072	cagaacttctatgatactaaatgtgcagtagcacagaagctccagaaaaaccagaat	7131
Db	22242	CAGACTTCTATGATTAACCTAAATGTGCCCGTACAGAGACTCCAAAGAAAAACCGAAT	22301
OY	7132	tgtttttgcaattcgccgagcatgtlaacccaagctctcaaatgtaacctcatgttaagt	7191
Db	22302	TTGTTTGTGCATTATGCGAGCATATACCCAGTCTCTTAATGTCACTTCATGATATGTT	22361
OY	7192	tgtgagaagaactgtataagaatgaatcaatg-cataagaagcccggaattagtgctaca	7250
Db	22362	TGTGAAAAAAC--TATATAAGAGATCAATGGGCATTAAGAAACCCAGAAATTAGTGGCTACA	22419
OY	7251	gaaccagttccctgatgatcccgccgccaagaatcaaccctgatacttctagttcta	7310
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OY	7311	aaagctcaattatagaacaatatgtcctagctgaaaaaagaagaatctcaatcact	7370
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OY	7371	gtagatgacttagtctgacctagacaaaaactgataaagtgtacc-----	7416
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OY	7471	aatttccaaagttagcagccgtttaaagcccccacagaattccaacgggaactagaacgcc	7530
Db	22659	AATTTCCAAAGTGTGAGACTATTATAGGCCACCCAGATTCACCCGGGACTGTGAC-GGCC	22717
OY	7531	cccactaagctatactgatacgttgacatagaacctaacgctaagctcctgacacagtgg	7590
Db	22718	CCCAACAGATTACTAATATATGCGAGACACACAGCTTATGCTAATCCTCGATACAGGG	22777

QY	751	acaggtatggtgttatttggcactataaacatcttcttccatcgccatacaata	750
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QY	7651	gggaactccgtgcttccctctctatgcttccgcgaagaagcgaatactgcatgat	7710
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QY	7771	agacacaagaatggcctaatggtataccagaccccaattacatgctcaactgaatcac	7830
Db	22952	AG-CATTAAGATGCGTCAACGAGATATC--GAACCCATCTCATCTCAACGATCATAG	2300
QY	7831	ggttgcaagctgttttagaataatcattacataaanaacgaatcaagccttgactcttg	7890
Db	23010	GGTTACAGGTGTTTATGAAATATTATCTAATAAATACGATCAAGTCTGACTGTTCTG	2306
QY	7891	ccgcgcaagaactcagataaagaatgcatctatcaaatatagattgctctgcactact	7950
Db	23070	CCGACGACGAGACTCGATGAGAAAAAATACATATATCAAAATAGCATGCTTGACTACT	2312
QY	7951	t-ctagcagctgaaagagaggtcatab-aaaattaaccttactaatctatgcttacaca	8008
Db	23130	TGCTACGACGTGAAGGAGAAATTTGTAGAAATTTAACTTACTTAATTTGTTGTTACACA	2318
QY	8009	tagtatactaaaggcaagtagttaaagaagtagttaagaatagtttaaaaactgacaa	8068
Db	23190	TAGATGATCAGAGGCAAGTGTGAGATATGTTTAAAGAAATA-----ACAA	2323
QY	8069	aacgycacatcgcgcgtacgagtgtaacagaga ttcgaccgcgaagccatggttagaa	8128
Db	23238	AACGCGACATGATACCTGTGSCAAGTGTGSCACAGACTCAATTCAGAGCACTGTTTGAA	2329
QY	8129	ggtygttccagcactaagagaattaaacctatataagagttataatagtaata	8188
Db	23298	ATTGTTGCCAGCAATAAAGATTTTAAA-----CTCTAAGATATTAATAGTAATAA	2335
QY	8189	aacctgttatctctcccttgccttgcctgctgcttacttcttaagtataaaagcttcat	8248
Db	23332	AACCTGTTACTCCTCCCTGTTGTGTACTGTACTTCTTTAAATATATAAGCTTCAT	2341
QY	8249	tgccacctatgttccacaaatgcccacaacaagtgcacata tgaatacactacatc	8308
Db	23412	CGCTACTTATGTTACCCAAATATGCTTCAGCACAATGTACTATTAATATCATCATCATC	2347
QY	8309	tattgcaagaagagcatalaagtggcaanaataagaatgagaatcccaactat-aaaag	8367
Db	23472	TATGTCACAAAAAGACATTAAGTAGCAAAAAATTAAGTAGAAGATCCACATTAATTAATAAG	2353
QY	8368	tggagatcttaaacgggggaaataggggagaagagagccctccatcatggttttatatc	8427
Db	23532	TGAATATCTCAAAAGGGGGAATAGAGGAAGAGAGAGCCTCTCAATATGTTTATATCT	2359
QY	8428	gtttatatctcagaagaagacagagaagcgaactcaagaagtagccggcgccctaaag	8487
Db	23592	CAGTACTGTTTAAAA-AAAAAAAAGTAAAAACCAAGACAGCCAGCTTGCGC-----	2364
QY	8488	aaccagacccgaacaacagagccctggcgctgcctgactaagcctgtagttaaatcgac	8547
Db	23645	--CCAGGCCGGAACCAAGGCGTGGGCGTGCCTGGCTTAACCCCGTAGTTAAAAATCAGC	2370
QY	8548	ccctgacctagcaaatggtgttactatagattccacaacatltgta tggaaagacattgty	8607
Db	23703	TCAATAACTTAG-AACCAATGTTATTCATAGATTCAGACATTTGATGAAGAACACTGTG	2376
QY	8608	aaatctctgtctgtctgcttcaactctgtgacaacacagtgctcaagccctctcaacgta	8667
Db	23762	AAATCCCTGCTTGTTCGTTTCTCTCTGTCCGTTGGTGCATGCACCCG--GTCAATGA	2381
QY	8668	ccccctgtacttcaatcgaatcacagacctcattagagaagcccccctaaagtgtgaaq	8727

Accession	Sequence	Position
Dd 23820	CCCCCTTGCTGCATCAATCAACCAACCCCTTTCATG-TGAATCTTACAGTTGTGAGC	23878
Qy 8728	ccctaaaggcagagaagttgagcacctctgacgagctgagatttgagacgctagcctgc	8787
Dd 23879	CCTTAAAAAGACACAGGAATTGTCTATGCAAGAGAACTCGGATTTTAAAGCAGTAGCTTGCC	23938
Qy 8788	gattcccaagctgtaattaaagcactccctcaactatcctgctgctcgaagggattctgc	8847
Dd 23939	AATACTCCACAGCTGATATAAGCC-CTTCCTTTACACACTACTCTCTGAGAAGTTTGTG	23997
Qy 8848	tgcagctgctcgtctgacactgta 8872	
Dd 23998	TGCGGCTGCTCTGCTACCATACCA 24022	

RESULT	12			
	HSDJ383p5/c			
LOCUS	HSDJ383p5	144304 bp	DNA	HFG
DEFINITION	Homo sapiens chromosome 6 clone RP3-383p5, *** SEQUENCING IN			
PROGRESS	***, in unordered pieces.			

ACCESSION	AL121947
VERSION	AL121947.2
KEYWORDS	GI:6249384
	HTG; HTGS_PHASE1.

ORGANISM	Homo sapiens
----------	--------------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 144304)

AUTHORS  
Slims, S.  
WITH DIRECT SUBMISSION

TITLE	DIRECT SUBMISSION
JOURNAL	Submitted (03-NOV

Cambridgeshire, C

**COMMENT**

hummer@esanger.ac.uk Clone requests: clonerequest@esanger.ac.uk  
on Nov 4, 1999 this sequence version replaced gi:6065993.  
IMPORTANT: This sequence is unfinished and does not necessarily  
represent the correct sequence. Work on the sequence is in progress  
and the release of this data is based on the understanding that the  
sequence may change as work continues. The sequence may be  
contaminated with foreign sequence from E. coli, yeast, vector,  
phage etc. Order of segments is not known; 800 n s separate  
segments. Unfinished: dj383p5 Contig\_ID: 00075 acc-AL121947  
Length: 5465 bp Unfinished: dj383p5 Contig\_ID: 00226 acc-AL121947  
Length: 22864 bp Unfinished: dj383p5 Contig\_ID: 00295  
acc-AL121947 Length: 1888 bp Unfinished: dj383p5 Contig\_ID: 00462  
acc-AL121947 Length: 1441 bp Unfinished: dj383p5 Contig\_ID: 00641  
acc-AL121947 Length: 7093 bp Unfinished: dj383p5  
Contig\_ID: 00674 acc-AL121947 Length: 17627 bp Unfinished:  
dj383p5 Contig\_ID: 00685 acc-AL121947 Length: 18337 bp  
Unfinished: dj383p5 Contig\_ID: 00773 acc-AL121947 Length: 1691  
bp Unfinished: dj383p5 Contig\_ID: 00977 acc-AL121947 Length: 6288  
bp Unfinished: dj383p5 Contig\_ID: 00989 acc-AL121947  
Length: 8255 bp Unfinished: dj383p5 Contig\_ID: 01366  
acc-AL121947 Length: 14979 bp Unfinished: dj383p5 Contig\_ID: 01393  
acc-AL121947 Length: 3141 bp Unfinished: dj383p5 Contig\_ID: 01397  
acc-AL121947 Length: 6571 bp Unfinished: dj383p5 Contig\_ID: 01522  
acc-AL121947 Length: 5549 bp Unfinished: dj383p5  
Contig\_ID: 01640 acc-AL121947 Length: 6069 bp Unfinished: dj383p5  
Contig\_ID: 01720 acc-AL121947 Length: 5056 bp.  
\* NOTE: This is a 'working draft' sequence.  
\* This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

### FEATURES

Location/qualifiers

**source**

BASE COUNT	ORIGIN
41164 a	25547 g 40331 t 12005 others

Query Match	10.3%;	Score 2559.6;	DB 32;	Length 144304;
Best Local Similarity	69.3%;	Pred. No. 0;		
Matches 4901;	Conservative	0;	Mismatches 824;	Indels 1347;
				Gaps 50;

[illegible]



OY 3788 attcctaacccagtaaccacagatgcccagatgcatcattcaatctgttagcaagctgct 3847  
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Db 27591 ATCCTTGACCCAGTAACCTGTGTGATGGCCCAATGCATTCAATTGTGTGCAACTGCT 27552  
OY 3848 ttgtcaacagagaaaaa----- 3873  
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Db 27531 TTGCTAACAGAAAAAGTAAGAAAAAACTTTAGAGAAACCTCATTTGTGAGCA 27472  
OY 3873 -----agagctgtggaagcaaa-----attt 3895  
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Db 27471 CACCTCACTAGTTCACTTCAGCTCAGGCTATCTTAATCATAAAAAGCCAAAAAGTAGCTTACTA 27412  
OY 3896 atgtaaagagtgctataatgtaaatctgtcttgaataatata----- 3944  
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Db 27411 ACTCAAAATCTTAATAATGTGGGCTATTCTGTAGAAAAAAAGAAAGTAATCCCTT 27352  
OY 3944 -----ctgtgtttaaagaaagaaataattgtataagtcagaaagtgagacat 3993  
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Db 27351 AACCCAGAGGTTTCTTAACAAGGATTTAATCTTAATACCATTAACAAGGCCAACCA 27292  
OY 3994 gtcaagaataatctgc-----gaaagtacata 4020  
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Db 27291 GACCTAAGAGAACTCCCTTCAGAGAGATGATGATGCTCTCCAGGTAATTGAA 27232  
OY 4021 gaaacagtgctataaa---aaattatgcaaaaatattgtataattggaagtaataa 4077  
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Db 27231 AAAAAAAGGTTATTAAGAAATTCATGCAGAAATGTTGTATATTTAAAGTAATTA 27112  
OY 4078 ggcctcctgagt---actatgaaagaaacagttatgtgcaagtgacataagaag 4132  
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Db 27111 GGCCTCCTTAATGTAAACCTATTAAGAAACAGTTTATGTGCAAGGTATATAAGAAAT 27112  
OY 4133 aaaaataccttggtaaaaag-attagaagagacataagaatgtgtaatttccctac 4191  
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Db 27111 AAAAATATCTTCTAGTAAGTAAGAAATTAAGAGCCATAGAAATGTAAGCTTTACCTAC 27052  
OY 4192 attaaaggttttaaaaaa----catgtttgaaagtttaagaagttttaaagt 4246  
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Db 27051 ATTTAAAGGTTTAAATATGTAATTTGTTTAAAGTTTAAATCAAGTTTAAATGTT 26992  
OY 4247 aattgtaaaaaaaattctgtgtgtaaacataatgtaagataaaaaagttatccca 4306  
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Db 26991 AATG-AAAAAAATCTGTGTGTAGAC--ATTGCCAAAGTTAAAGGATCATCA 26936  
OY 4307 gtttctcgtgaactgagcaataaagtaaaatgcaacaggttcttctggaagcccaac 4366  
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Db 26935 GTTTTCTGTAAACTGGACATTAATAAGCATTAACAGGTTTCTTAAACACAAAC 26876  
OY 4367 ctgctcttaacaaaattataaaaggttaaaagagctctgtaaaacttactatggt 4426  
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Db 26875 CTGCTCTTAGCAAAATATTAAGTTAAAGTTAAAGAAATCTATTAATCTTACTTATGAT 26816  
OY 4427 caaacatgaaaaaattgtaaaatgtaaatgtaagtttatataaaattgaattacaat 4486  
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Db 26815 CAAATATTAATAATGATGAATA--ATGCTACAAAGTTTATTAATAATTAAGTTTAACAT 26758  
OY 4487 aataacacataataaagtaaaattagctatctggtataaaatcatacaagaag 4546  
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Db 26757 AATAACACACTAATTAATTAATGTAATTAATTAATCTGCTAATAAAACATACAGGAAG 26698  
OY 4547 tatataataataaataatggtgtttagcttcttctggtctaaataataaataag 4606  
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Db 26697 CATGTTTAATGTAATAATGATTTGCTTTCTTGTGTTAAACCTATATAAATAGT 26658  
OY 4607 cctaaagaa----- 4617  
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Db 26637 GCTTAAGGAAATTTCTCAGTAATAAAAGCACTAAGACTATAAGTCCACCAAGTCC 26578  
OY 4617 ----- 4617  
Db 26577 CCACATTTAAACAAAGATCAATTTCTTAATAATTAATACTGTGTTATCTTCCACTT 26518  
OY 4617 ----- 4617

Db 26517 TCCTTCCCTCAAAAAGTCTTTAGCACTGTGACACACCTTAGAAATTCGGSTA 26458  
OY 4617 ----- 4617  
Db 26457 AACAGAGCACCCCTGAAGATCACGTTCTGTCAAAGGTGGAAAGAAAACTCGAG 26398  
OY 4617 ----- 4617  
Db 26397 CCAGCCTAAGAGACCTTACCTTGTCTGCTAACCCAGAAATGCTTTCATACAGCA 26338  
OY 4617 ----- 4617  
Db 26337 AAAAGGATAGATCATGATGCCGACCTCAAGAAAGGCCACCCCTCAGAGTGTGG 26278  
OY 4617 ----- 4617  
Db 26277 CCATAGTCCAGGGGAAACCTACCAACTAAGCTAAGAAAAATTAAGTGTTCAT 26218  
OY 4617 ----- 4617  
Db 26217 CTAGCTATTACTCTTTCTTTCTCTGTTATGCTGACCATCTAGTTATTACATA 26158  
OY 4617 ----- 4617  
Db 26157 ACCAGTCAATTTGCCCTCAAACTATTGCATCTATGCTTGCTGTGAGACTGCCAA 26098  
OY 4617 ----- 4617  
Db 26097 GTCAAGACAGTTTCTACTTCAGAAAAAGTACTTCTCTCTGACTCTCTTAGACT 26038  
OY 4617 ----- 4617  
Db 26037 GGGCATTAAGTAACTAGACCATTTAATCGGGGAGATTGTGAATAAGACCCAGTCCG 25978  
OY 4617 ----- 4617  
Db 25977 ACCAGAGCTTTGCCCCGATGTAGACTTTTCATGCCATAGTTGTGTCACATCTGTG 25918  
OY 4617 -----a 4617  
Db 25917 GACCACTAAGAGCAAGATGAGTCCCCCAACAGTTTGTAAATTTCTTAATCATTA 25858  
OY 4618 catattattactagagatcatagaagttaaagctaaacaaacttggcaattag 4677  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 25857 CATTAATTTACTAGAGATGATGAAGTTAAAGCTTAACAACAACCTTAGCAATTAG 25798  
OY 4678 acagataccaagatgcaaatgacctggttgaatgtaataatattccatctgacatca 4737  
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Db 25797 ACAGATACCAAGATGCAAAATGCTGTTAAATGATCAATATTCATCTGCATGTTA 25738  
OY 4738 aaaaaagcagttgtatgtctgtgtgcaatgcaagcagagccctcatatgtccctt 4797  
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Db 25737 AACAAAGCAATTTGTTATGCTGTGACATGAGGAGCCAGAGCCCAATGTCCTCCCTC 25678  
OY 4798 ccactaaagtgctctcaagccaacagcggtggtgctgcatagtgtaagctctttccagat 4857  
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Db 25677 CCACCTAAGGTGCTCTCAGTGACATGATAGGCTCAATGATGCTTTTCCGAT 25618  
OY 4858 tctacagcctgagtaataatgcatgccaactctctctgcat----- 4902  
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Db 25617 TCTACAGCTGAGTAATTAAGTCAATGCCAAGCTCTGTCTATCCGAAGTGTGCA 25558  
OY 4902 cccgtgtggtcaagcccccgaagggcatccagctccgtctcccaactaagtctacttc 4961  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 25557 CCTTCGGTTGAGCTGCAAGAGGCCATCCACCTTCATCTCCCAACATAGTTCATCTC 25498  
OY 4962 atgtctcacacagagagaaacttagagttccttggagaccctgaagtcatgcaatga 5021  
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Db 25497 ATGTCCTCATGACAGGAGGAAA--TAGCATTTCTTGTGAACCTGAAAGGATGTGATGA 25440  
OY 5022 gcttaagaatttcaagagcttaaatcaatcagtcagccctgttcatcccaagcgagatg 5081  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

D	b	25439	gTTTAAGAAATTTTCAAGAGCTTATATCAATCAGTCAGACCCCTGTGTTCAATCCCCAGAGTGAGATG	25380
Q	y	5082	gtGgtgtagtattggtgtggaaccttaactggtgacactgtccgaataactgtagtggcaactta	5141
D	b	25379	gtGGtggTATTTGTGGTGAGACCTTTACTGGGCACTGTGCCAATAATACAGAGGGCACTTG	25320
Q	y	5142	tactttagTcccaagtttgggtcatatccctttcaacccctgtgcattcttaacaagagggagaa	5201
D	b	25319	TCCTTTAGCCATGTGGCTGCTCCCTTTTACCTGGCATTTCATCAACAGAGAGTGGAAAA	25260
Q	y	5202	aaTaagacaTgtlaaagcgaagaagcccccttaaggtccttgcaacttcagctcagTccat	5261
D	b	25259	AATTAAGACATCTAATAAAGCGGGAAG-CCCTTATGGGCTTTCAACTCTCACTCATCTATT	25201
Q	y	5262	tagacgcaattgtagtTcccaaggaataccagatcaatlaaagcttgaactgaataag	5321
D	b	25200	TGATGTGCAATTTGGAGCCCTGCAAGGAATACAGATCAATTTAAAGCTTGAATCAAAATAG	25141
Q	y	5322	ctcaaaaatttaagTcaaatctttgttgtagta-gttaataaaaatgtaattagataa	5380
D	b	25140	CTACAGGATTTAAGTCAAATATTTTATGTGGTACAGTTATATAAATGATGATTGATPA	25081
Q	y	5381	attatactatttacaacaacacagcaacaagctttcatagtttgaagaanaaacTcaagt	5440
D	b	25080	ACTACATCTATTACAACCAACGACAAACAAAGCTTTTCATGATGATTAAGAANAACTCATGT	25021
Q	y	5441	ggggcccaagcccttgggtgtactctgaactgaagaagtgcacactatgtgtccaaaaaa	5500
D	b	25020	CGGCTTCATCTCTGGGGCTACCTGACCTGCACAAACCCCTTTTACCCTCATGTGTCA---	24964
Q	y	5501	aaaaaaaaaaaaagggcatactataccaattcttaagttaattagactaaacaagTct	5560
D	b	24964	-----	24964
Q	y	5561	tactataTgcaaggaataatltgaatTcccaacttacaagTttcaacaagaatlaagt	5620
D	b	24964	-----	24964
Q	y	5621	ttgttaaaagttaacagTgtlaacatgtattatagtaacttaactctgttgcccttagac	5680
D	b	24964	-----	24964
Q	y	5681	agTctagTccacagataataagaagttcacttaaaaaaataaaaaaagaatgtttatc	5740
D	b	24964	-----	24964
Q	y	5741	tcaaaaaaanaaaatgTcagtttgagtttaaccagaactgtaagTctgtgccaagc	5800
D	b	24964	--GAAAAAATAAATGCGAGTTGGAGTTTAAACCAAGCTGTAGGGCGCTGGCAAAAGC	24907
Q	y	5801	caTgTcctatctTcnaaaacaactagatgTgggtttccaaagTcTgccccatactaa	5860
D	b	24906	CAGTGGCTATCTCTCAAAACAATAGATGAGGGGTTTCCAAAAGCTGGCCCCATGTAA	24847
Q	y	5861	ggggccctTgTcagcaagTccctgttagcaacaagaagcagataagTtaactcttagTcaaa	5920
D	b	24846	GGGCGCTGGCAACATGGCTTGTTAGGCAAGAAAGCAGATTAAGCTAATCTTTAGGCAAA	24787
Q	y	5921	acctaaacaTaaagTccccccatgtctgtgtgTgacttaatcagTaaacaagaagTaat	5980
D	b	24786	ACCTTAAACCTTAAGT-ACCCCATGTGTGGTGACTTTATATAATCCMAAGCATCAT	24728
Q	y	5981	tagctaatTaaTgTcagacttaactagataccaaagctgtctgtTgaaatccccacata	6040
D	b	24727	TAGCTATATTAATGCTTAGACTAATCTAGATATCAAAGCTTGATTTATGAAATCCCGCAT	24668
Q	y	6041	accatTgaagTttgcaacacccTaaaccccgTcacctgtctctgtTlacagagaTcca	6100
D	b	24667	ACCATTTGAAGTTTACAACACCCCTAAACCCGCGACCTTCTCTGTATCAAGAGCCCA	24608
Q	y	6101	gtTaaacataactgtgttagaagTgttgaaTcagttatctatgtgtggccaactccaa	6160
D	b	24607	gTTTGAACATTAACCTGTATAGAGTATTTGGACTCAGTTTATCTTAGTGGGCCCACTTCC-A	24549

QY	6161	aaccatccttaacatcagtaactcggagcgtctgacgtcgtgatacgtggagacagccttaccac	6220
Db	24548	AACCAATCCCTTAACAGCAGTAACCTGAGAGCTGTACGTGATGGAGCGCTTCACCAAC	24489
QY	6221	ctctgcaaaagttaacc-----agaaaaacccctgtctccagtcacacccggaagtga	6272
Db	24488	CCCTGCAAAAGTGGCTCTGTGAAGAAAGATTAAACAACCCCTGCTTACGTACACACTGGAAAGCTGA	24429
QY	6273	ctgtctccagcagcagccggaagcatagaanaactcatcacagggaactcaatttccttaaat	6332
Db	24428	CTGGTCCAAAGCAGCGCCGGAAGATGAGGAATACTATCACGGGACATATTTCTTTAAAAA	24365
QY	6333	ttagagctgtacagtaagaagacttcaacttacctctctcagacttggaagactgtctccagta	6392
Db	24366	CTGGACTTGTACAGTAAGAGACTTCAACTGACTCTCTCTCAGACTGAGGGCTGTTCCTAGTG	24309
QY	6393	tatataccaagtcactgaagctagaagcaaaaagattgtctacagtcctattatltcatggtta	6452
Db	24308	TATACATCTATGTCACTGAGGTGGAGCAAAAATTTCTACGGTCCATATTTTAACAGTTA	24249
QY	6453	ttataagctgtacaggaagccttaaaaagaaactgtttgtataatgtcatcttcaacaagt	6512
Db	24248	TATATAGTGTACTGGAACCTTAAAAAGAACTGTTTGTATATGTTACTCTATACAGGT	24189
QY	6513	atgtagccttaggaaataaccaactgtatgtgtgtatgaaccatttaaagcctccaatga	6572
Db	24188	ATGTAGCCCGAGAAATGACCAACCTTAAGTGTGTATGACCCA-TCGTAGCCCTCCATGA	24130
QY	6573	tcaaggtttttaaataataataaagagct-----gtccctttcagttgacacaa	6623
Db	24129	CCACAGTTTAAAAATTAAAGTTTAAGATTAAGAACTGAAGACTGGTGGGGGCTCATTAACGATATGA	24070
QY	6624	gtaaagtaataagctaaagacagaagaagaaggaatccccaagcatgtlaacactataatla	6683
Db	24069	GTAAGGTGTATCCCAAAACAGAAAAAAGAGAGTCCCAAAATGAATACACTTGAAGATTGG	24010
QY	6684	atgcttgtgcccctatccaatagcactcggaataagaatgagtggtttcttaactgaa	6743
Db	24009	ATGCGCTGTGCTGTCTATTATATATTAAGTTAGAAATAGAGATGTGGTCTCTTAATT---	23952
QY	6744	aaaaaaaagtctacacagcaagaataagtaatactcgcacgaataataagccatgtgca	6803
Db	23952	-AAGAAAGAGGCTATATATGSCAANAATAAGTACGTTTATCAATAATTAAAGCTGTGTAA	23894
QY	6804	aatgtgtgtaactactgctgtctgtgcactagctagctactaga-aaaagatgaaanaaga	6862
Db	23893	AATTAATATGTGATCTGTGCTCATCTCATATTGTAGGCTACTTGATTAATAAAAAATGA	23834
QY	6863	cccttcttagagcccaaaaaagsgaagsgaagcccctcctgttaagagtgsgaagctgaaccc	6922
Db	23833	TCTGTGCCCTTCAGCAAGGAGAAAGTGCGCCCTTCTGTACAGTGGGCTAGTGAACCC	23774
QY	6923	cttgaatattgaattactacaatcccttlaaacccaaggtagaanaaaaagaatfacacgtat	6982
Db	23773	CTTAGACTAGTAATATACCAACCCCTTAATATCTGTGCTAG-AAAAAAGGGAACGCTGA	23715
QY	6983	ctctgtggcgctgataaaaaagactagatcctagagtaatactccttagtaaaagsgag	7042
Db	23714	CCCTAGAAATTGATGTGAGCTGAAATGGAATCTTCAAGTAAATATCTGTGTTTAGGAAAG	23655
QY	7043	ttcgtgaactctctcggaaaccaagatctcagacttctatgaatttaactaaatgtgcccag	7102
Db	23654	TTTATTAACGCTCTCTCTGAGCATTATTTCAACCTTCTATGATATACAGTAAGATGA	23595
QY	7103	taccagagagactccaggaanaaacagaanaattgttttgcatttagccgagcatgtagccc	7162
Db	23594	TACCAAGAAATTCCAGAGAAAAACAABAANTTTTGTTCGAATTTACTGTACATGTAGCCC	23535
QY	7163	agctctctaagtcaacctcatgttactgcttltgtgsgaanaactgtlaaagaagatcaatg-	7222
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OY	7222	caaaagaagcccgagaaattagygcccaagaccacccattccctcgtatgatcccggc - ccaa	7280
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RESULT 13  
AC003983/c

LOCUS	AC003983	105563 bp	DNA	PI1	13-JAN-1998
DEFINITION	Human PAC clone DJ0093103 from Xq23, complete sequence.				
ACCESSION	AC003983				
VERSION	AC003983.1	GI:2769694			
KEYWORDS	HTG.				
SOURCE	human.				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 105563)  
Tln-Mollan, A., Hinds, K., McDonald, R. and Ozersky, P.  
The sequence of H. sapiens PAC clone DJ0093103  
Unpublished (1998)  
2 (bases 1 to 105563)  
Waterston, R.  
Direct Submission  
Submitted (13-JAN-1998) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
SUBMITTED BY:  
Genome Sequencing Center  
Department of Genetics  
Washington University  
St. Louis MO 63108, USA  
<http://genome.wustl.edu/gsc>  
<mailto:sapiens@watson.wustl.edu>

COMMENT  
JOURNAL

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded or sequenced with an alternate  
chemistry; an attempt was made to resolve all sequencing problems,  
such as compressions and repeats; all regions were covered by  
sequence from more than one subclone; and the assembly was  
confirmed by restriction digest.

## MAPING INFORMATION:

This sequence was generated from part of bacterial clone contigs of  
human chromosome X, constructed by David Bentley's chromosome X  
mapping group at the Sanger Centre, Wellcome Trust Genome Campus,  
Hinxton, UK. Further information can be found at  
<http://www.sanger.ac.uk/HGP/ChrX>

## SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-1, prepared by  
Pieter de Jong and coworkers at Roswell Park Cancer Institute,  
using the method described by Ioannou et al., Nature Genetics  
6:84-9 (1994). The library is from one male donor. For further  
details, see <http://bacpac.med.buffalo.edu/>  
The clone is available from Genome Systems, Inc.  
(<http://www.genomesystems.com>).

VECTOR: pCYPAC2

## NEIGHBORING SEQUENCE INFORMATION:

The actual start of this clone is at base position 1 of DJ0093103;  
actual end is at 105563 of DJ0093103. The orientation of this clone  
is unknown.

This clone contains a single stranded region from 83424-83427.

## FEATURES

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## RESULT 14

AC006047

LOCUS AC006047 37139 bp DNA PRI 24-NOV-1998

DEFINITION Homo sapiens clone UMGC:Y14C057 from 6p21, complete sequence.

AC006047

VERSION AC006047.1 GI:3924651

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

1 (bases 1 to 37139)

Gulliaudoux, T., Janer, M., Mong, G.-K., Splies, T. and Geraghty, D.E.

The complete genomic sequence of 424,015 bp at the centromeric end

of the HLA class I region: gene content and polymorphism

Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9494-9499 (1998)

JOURNAL

MEDLINE

REMARK

Fred Hutchinson Cancer Research Center

The Clinical Research Division

1100 Fairview Ave. N., P.O. Box 19024

Seattle, WA 98109-1024

2 (bases 1 to 37139)

Geraghty, D.E. and Olson, M.V.

Direct Submission

Submitted (24-NOV-1998) Human Genome Center, University of

Washington, Box 352145, Seattle, WA 98195, USA

Overlapping Sequences:

5': UMGC:Y14C094 (Genbank Accession: AC004185)

3': UMGC:Y24C027

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Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

Genbank flat file format but are available as part

of this entry's ASN.1 file.

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Double stranded (DS) coverage: 79.7%

DS or two chemistry coverage: 99.9%

Single stranded regions: 2

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Sequence Validation:

This sequence has been validated by Multiple Complete Digest

Mapping. Comparison of the experimentally derived map digest

fragments with sequence-predicted fragments is given below.

Small fragments below a variable cutoff (approximately 400-600bp)

are not mapped and hence do not appear in the table. There are no

significant remaining discrepancies between the experimental and

predicted values. Uniquely ordered fragment groups are separated

by dashed lines.

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Map Seq Map Seq Map Seq

BgIII HindIII NsiI

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2295.76 2284.00 9892.52 9705.00 12663.41 12695.00

23644.64 24046.00 4849.02 4754.00 1503.72 1496.00

979.90 957.00 2968.55 2927.00

3644.92 3580.00 1732.43 1722.00

4622.81 4524.00

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## FEATURES

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Location/Qualifiers

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1671.85 1648.00



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D57470 TTAATAATTAATTAATTAATTAATTAACACATTAATTAAGTAAATAATTAATTAATTA 57529  
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Db 59494 GCGTTCCTAAATGGAAGAGACAGTAAAGTAAAGTATCTGTC 59553
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Db 59554 AAGAATTGTATTATGTG--AGATGTGCAATACTGCTCTGTGTCAATTGGCTACTT 59610
Oy 6844 agaaaagatgaaaagaccctgtttagc 6873
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Db 59611 AAAAAAGAGATAAAAAGATCCTCTTTGGC 59640

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Search completed: February 29, 2000, 20:12:08  
 Job time: 118599 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2000, 11:15:29 ; Search time 20117.6 Seconds  
(without alignments)  
-3018.640 Million cell updates/sec

Title: US-09-339-352-7\_COPY\_1\_20000  
Perfect score: 20000  
Sequence: 1 gacatctctcttcagggcc.....gaaactagatctcttga 20000

Scoring table: IDENTITY\_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl.\*

Word size: 0

Number of hits that pass the threshold: 1642386

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2: gb\_dai.\*  
3: gb\_om.\*  
4: gb\_om.\*  
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6: gb\_ph.\*  
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48: gb\_ph.\*  
49: gb\_ph.\*

50: gb\_pl3.\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20000	100.0	102258	11	HS295C6	297876 Human DNA s
2	5877.2	29.4	128230	11	HS31314	299943 Human DNA s
3	1744	8.7	7728	11	AF058907	AF058907 Homo sapi
4	1701	8.5	135305	11	HS71113D6	AL0808317 Human DNA
5	1646.8	8.2	137413	42	AC011036	AL011036 Homo sapi
6	1611.8	8.1	138088	43	AC010877	AC010877 Homo sapi
7	1586.6	7.9	158463	44	AC011019	AC011019 Homo sapi
8	1560.8	7.8	227567	42	AC008554	AC008554 Homo sapi
9	1517.8	7.6	226345	40	AC005406	AC005406 Homo sapi
10	1442.6	7.2	36921	40	AC004185	AC004185 Homo sapi
11	1442.6	7.2	37139	40	AC006047	AC006047 Homo sapi
12	1430.2	7.2	100000	10	AP000509	AP000509 Homo sapi
13	1430.2	7.2	236822	10	D84394	D84394 Homo sapien
14	1392.6	7.0	97906	32	HS45466	AL109912 Homo sapi
15	1381.8	6.9	79376	11	HS45466	298750 Human DNA s
16	1341.4	6.7	174768	41	AC009330	AC009330 Homo sapi
17	1339.2	6.7	161428	41	AC009542	AC009542 Homo sapi
18	1337	6.7	182011	33	AC007683	AC007683 Homo sapi
19	1331.2	6.7	191235	42	AC012487	AC012487 Homo sapi
20	1250.2	6.3	105563	11	AC003983	AC003983 Human PAC
21	1230.6	6.1	163738	42	AC009505	AC009505 Homo sapi
22	1100.4	5.5	200607	44	AC016775	AC016775 Homo sapi
23	1082.8	5.4	173157	42	AC011895	AC011895 Homo sapi
24	1081.2	5.4	203488	42	AC009468	AC009468 Homo sapi
25	1020.4	5.1	129480	41	AC008428	AC008428 Homo sapi
26	961.4	4.8	110409	42	AC010487	AC010487 Homo sapi
27	914.2	4.6	268399	33	AC004469	AC004469 Homo sapi
28	901.4	4.5	144304	32	HS0383P5	AL121947 Homo sapi
29	882.2	4.4	123585	11	AC004707	AC004707 Homo sapi
30	870.4	4.4	167932	41	AC008687	AC008687 Homo sapi
31	867.6	4.3	122000	11	AC003093	AC003093 Human BAC
32	837.4	4.2	59380	42	AC010521	AC010521 Homo sapi
33	836.2	4.2	118226	11	HS46618	AL030988 Homo sapi
34	834.6	4.2	158810	44	AC011604	AC011604 Homo sapi
35	819.2	4.1	142552	11	HS58128	AL035410 Human DNA
36	818.4	4.1	76340	11	AC003678	AC003678 Homo sapi
37	815.2	4.1	137693	40	AC003689	AC003689 Homo sapi
38	812	4.1	149876	32	AP000437	AP000437 Homo sapi
39	812	4.1	131922	32	AP000589	AP000589 Homo sapi
40	809.6	4.0	151600	43	AC011682	AC011682 Homo sapi
41	793.6	4.0	171636	10	HS215K18	Z83820 Human DNA s
42	792.8	4.0	192334	40	AC007319	AC007319 Homo sapi
43	781.8	3.9	132805	11	HS339A18	Z97054 Human DNA s
44	774	3.9	214717	44	AC016759	AC016759 Homo sapi
45	770.4	3.9	113853	40	AF196971	AF196971 Homo sapi

## ALIGNMENTS

RESULT 1  
LOCUS HS295C6 102258 bp DNA PRI 23-NOV-1999  
DEFINITION Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STR and Cpg island.  
ACCESSION Z97876  
VERSION Z97876.1 GI:2582745  
KEYWORDS 1q24; Cpg island; repeat polymorphism.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 102258)  
AUTHORS Grafham,D.  
TITLE Direct Submission  
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk  
On Nov 2, 1997 this sequence version replaced g1:2465042.  
IMPORTANT: This sequence is the entire insert of clone 295C6.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variations annotated may not be found in the sequence submission  
corresponding to the overlapping clone as we submit sequences with  
only a small overlap as described above.  
This sequence was generated from part of bacterial clone contigs of  
human chromosome 1, constructed by the Sanger Centre chromosome 1  
mapping group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1/  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key  
The true left end of clone 295C6 is at 1 in this sequence. The true  
right end of clone 295C6 is at 102258.  
295C6 is from the library RPCII constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong.  
For further details see http://bacpac.med.buffalo.edu/  
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2612..2903  
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223618"  
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4969..5140  
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5146..5448  
/note="AluJo repeat: matches 302. .1 of consensus"  
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/note="AluSg repeat: matches 1. .299 of consensus"  
repeat\_region  
5797..5925  
/note="MER42c repeat: matches 1265. .1124 of consensus"  
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/note="THELC repeat: matches 1. .371 of consensus"  
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16144..16585  
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17173..17534  
/note="LTR2 repeat: matches 105. .449 of consensus"  
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AA300207; match: W37181 N52820 AA337499 W87891 H84729;  
similar to endogenous retrovirus POL POLYPROTEIN"  
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repeat\_region  
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repeat\_region  
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29517..29629  
/note="MIR repeat: matches 262. .151 of consensus"  
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29631..29928  
/note="AluY repeat: matches 1. .295 of consensus"  
repeat\_region  
29937..30237  
/note="AluSg repeat: matches 1. .301 of consensus"  
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30238..30315  
/note="MIR repeat: matches 158. .76 of consensus"  
repeat\_region  
31096..31287  
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repeat\_region  
31289..31379  
/note="MIR2 repeat: matches 146. .56 of consensus"  
repeat\_region  
31479..31525  
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/note="MIR repeat: matches 9. .253 of consensus"  
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33565..35744  
/note="MIR repeat: matches 262. .74 of consensus"  
repeat\_region  
36165..36466  
/note="AluSx repeat: matches 1. .302 of consensus"  
repeat\_region  
36692..36944  
/note="MIR repeat: matches 3. .240 of consensus"  
repeat\_region  
36999..37299  
/note="AluSx repeat: matches 301. .1 of consensus"  
repeat\_region  
37924..38114  
/note="L1MA2 repeat: matches 1055. .866 of consensus"

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	repeat_region	38479. .3857	/note="L1MA2 repeat: matches 874. .687 of consensus"	
	repeat_region	3858. .38957	/note="AlusX repeat: matches 300. .1 of consensus"	
	repeat_region	38958. .39580	/note="L1MA3 repeat: matches 699. .85 of consensus"	
	repeat_region	39585. .39875	/note="AlusX repeat: matches 292. .1 of consensus"	
	repeat_region	39877. .39951	/note="L1MA9 repeat: matches 88. .14 of consensus"	
	repeat_region	39944. .40919	/note="L1 repeat: matches 4416. .5300 of consensus"	
	repeat_region	40769. .41662	/note="L1PA2 repeat: matches 1. .893 of consensus"	
	repeat_region	41764. .42556	/note="L1 repeat: matches 5133. .4305 of consensus"	
	repeat_region	42557. .42857	/note="AluY repeat: matches 1. .301 of consensus"	
	repeat_region	42876. .43925	/note="L1 repeat: matches 4313. .3215 of consensus"	
	repeat_region	44235. .44498	/note="MER43 repeat: matches 3. .272 of consensus"	
	repeat_region	44788. .44860	/note="MIR repeat: matches 154. .82 of consensus"	
	repeat_region	44933. .45220	/note="AlusX repeat: matches 289. .2 of consensus"	
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	repeat_region	47393. .47677	/note="AlusX repeat: matches 1. .302 of consensus"	
	repeat_region	48309. .48404	/note="MIR repeat: matches 48. .140 of consensus"	
	repeat_region	48620. .48862	/note="MER21B repeat: matches 347. .102 of consensus"	
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QY	241	cacacagtagaanaactagttattatcttataataatagctgattataatagagcag	300	
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[illegible]

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Dh	18961	AATATTGTAATAGTCAGAAAGTTGAGCAATGTCAAAGAAATTATCTCGGAAGTCATAG	19020
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Dh	19021	AAAAGCATGTTTAAAAAATTATTCACAAAAAATTGTATTAATTTGAAAGTATTAAGCC	19080
Oy	19081	tccctgactactcttgaagaaacacgcttattgtgtcaaggtgtcetaaagaaagtataatc	19140
Dh	19081	TCCTAGATACATATTAAGAAACAGTTATATGTCCAAAGTGTCAATAGAAAGTAAATATAC	19140
Oy	19141	tttctgtataaaagatlaagaaggacataagaattgtgaattttacactacataaaggt	19200
Dh	19141	TTTTGTAAAAAAGATTAGAAGAGGACATAGAAATGTGATTTTACCTCATTAATAAGST	19200
Oy	19201	taaaaaaattatgtcttggaaagtttaagcaagttttaaattgttaattgtataaaaaa	19260
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Oy	19261	ttctgtgttaaaccaattagcttaagaataaaagatcatccagtttctgtgaact	19320
Dh	19261	TTCTGTGTATACCAATATTAGCTAAAGATAAAGATATCATCCAGTTTCTGTGAACT	19320
Oy	19321	ggacatlaaaglaaanaatgcaacaggtttctctgaagcacaacctgtctttaacaa	19380
Dh	19321	GGACATTTAAAGTAAAAATGCAACAGGTTTCTTGAAAGCCCAACCTGCTTTTAAACA	19380
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Dh	19681	CATACCAGATGCCAATGTCTGTTGAATGATCAAAATATTCATCTGCACTTTAAACA	19740
Oy	19741	aaagaagtgttatctctgtgtgacgttgagagccagaagcccttatgtcccccttcac	19800
Dh	19741	AAAGAGTGTATCTTGTGTGACATAGGAGGCCAGAGCCCTCATATGTCCCTTCCAC	19800
Oy	19801	taaagtgtccctccagctccacacagcgtygggtgacatgttagctctttccagaattcta	19860
Dh	19801	TAAATGTGCTCCACAGTCCACAGGCGTGTGCATGTACTCTTTTCCAGATTTCTA	19860
Oy	19861	cagccttgagtaataagtaatgcacaaactctctgtctatcccttgygttcagcccccga	19920
Dh	19861	CAGCTTGAGTATTAAGTATAGTCACAAACTCTCTGTCTATCCCTGTGGGTGAGCCCCGA	19920
Oy	19921	gggcatccagcctccgtctcccaacaataagttcaactcatagtctctcaacagagag	19980
Dh	19921	GGGCATCCAGCCTCGCTCCCAACACTAAATTTCACTTCATGTCTCTCCACACAGAGAG	19980
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LOCUS	HS313L4	128230 bp	DNA	PRI	23-NOV-1999
DEFINITION	HS313L4	Human DNA sequence from PAC 313L4 on chromosome 1q24. Contains ESTs.			
ACCESSION	299943				
VERSION	299943.1	GI:2887308			
KEYWORDS	1q24.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 128230)				
TITLE	Pearce,A.				
JOURNAL	Direct Submission				
COMMENT	Submitted (12-NOV-1997) Chromosome 1 Project Group (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humbri@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Feb 14, 1998 this sequence version replaced gi:2578084. IMPORTANT: This sequence is the entire insert of clone 313L4. During difference assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1/ This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 313L4 is at 1 in this sequence. The true left end of clone 295C6 is at 122337. The true right end of clone 313L4 is at 128230. 313L4 is from the library RPC11 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/. Location/Qualifiers				
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repeat_region	1781..2080				
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repeat_region	2081..2210				
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repeat_region	2692..2780				
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repeat_region	4630..4669				
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repeat_region 7732..8034
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repeat_region 29924..30226
/note="AlusX repeat: matches 299..1 of consensus"
repeat_region 30296..30594
/note="AlusX repeat: matches 301..2 of consensus"
repeat_region 31058..31167
/note="MERSB repeat: matches 31..134 of consensus"
repeat_region 31174..31438
/note="LIMC1 repeat: matches 1064..787 of consensus"
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38392..38604
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H08848; match: R64027 R39393 AA291124"
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repeat_region 41025..41616
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Matches 5891; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
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LOCUS	AF058907	
DEFINITION	Homo sapiens pleiotrophin (PTN) gene, exons UV3, UV2 and UV1.	
ACCESSION	AF058907 U71455	
VERSION	AF058907.1 GI:790543	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE	Schulte,A.M., Lai,S., Kurtz,A., Czubayko,F., Riegel,A.T. and	
JOURNAL	Wellstein,A.	
MEDLINE	Human trophoblast and choriocarcinoma expression of the growth	
REFERENCE	factor pleiotrophin attributable to germ-line insertion of an	
AUTHORS	endogenous retrovirus	
TITLE	Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14759-14764 (1996)	
JOURNAL	97121462	
MEDLINE	2 (bases 1 to 7728)	
REFERENCE	Schulte,A.M. and Wellstein,A.	
AUTHORS	Structure and phylogenetic analysis of an endogenous retrovirus	
TITLE	inserted into the human growth factor gene pleiotrophin	
JOURNAL	J. Virol. 72 (7), 6065-6072 (1998)	
MEDLINE	98285768	
REFERENCE	3 (bases 1 to 7728)	
AUTHORS	Schulte,A.M. and Wellstein,A.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-APR-1998) Pharmacology, Georgetown University Medical	
COMMENT	Center, 3970 Reservoir Road, Washington, D.C. 20007, USA	
FEATURES	On Oct 27, 1998 this sequence version replaced gi:11778411.	
SOURCE	Location/Qualifiers	
gene	1..7728	
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exon	/chromosome="7"	
LTR	/map="7q33-34"	
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[illegible]

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Db	1936	GCCTCGCCAGACCCCTGTGTGGCAGGCCCCCTGGAGATCAACCCAGTGCCTGAACAC	1995
Qy	17760	gggaagaga-----ttgcacttggagtcggacaactaaacttggtaagctagc	17812
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Qy	17813	tttggaaacttgcacacccatttgatgtgaagcatgacctgaatcaaccaagcgctgtcct	17872
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Qy	17926	tttttgggaacttgcacacccatttcccaacttccatttggatgtgaagacagctgtactga	17985
Db	2175	TTTGGGAACCTTGCCTACTCCATTC-----AAGTGAACCATGTC-----CTGA	2218
Qy	17986	tcaccacagctgtgcctgttccgcagcatttggtttctgttcttgcacttgaatgctgc	18045
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Qy	18106	tgaatttggtttaagtgaatcaacgcgaagaagtgtgtgtgtgtgtgtgtgtgtgtgtgt	18155
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Qy	18405	tggcaaaagttaactgttaagccaagagcacaagaccagtttctgtacatagaacatca	18464
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Qy	18511	gaagaagagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga	18555
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Dd	2939	AGAGGAGACGACAAAGTCTAAAGAGAGAAAGCAACAAAGAGAGAGAAATATCCAGTAATCTAA	2998
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Dd	2999	GAAATAATACAAATATACCTGTAAT-CCCTTTAAAGGCCAAGCATTTTAAACCTATATATG	3057
Qy	18684	ataattaaaggtatctccgttaaccctctgaacacttaacttaacacttctgttaagtga	18743
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Qy	18744	aaccaagggcgtatcccgaaagcaacgtagggccttcctataaaaaatccttaeccagtaac	18802
Dd	3118	AACAAGGGGGGTATCCGGAAAGCACTGAGGCGCTTCATACAGAAACCTTAAACCCATAC	3177
Qy	18804	ccaagatctggccagatgatcatcgaatcgtgttagcaagcagctctgtctgaacggaaaaa	18865
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Qy	19158	gaagagggcaataagaatgtggatttttaccatcattaaaggtt--aaaaaatattgtt	19216
Dd	3777	TAAAGAGCATATAGATGTGGATTTTATACCTTCAATTTAAAGTTAAAAAAATCATTTGTT	3836
Qy	19217	ttgaaagtttaagcaagtttlaaaaatgttaactgttaaaaaaaaatctgtgtlaaacta	19278
Dd	3837	TTGAAGAGTTTAAGCAAGTTTAAAAAGCTTAATTTGT-AAAGAAAAATCTGTGTAAACAT	3895
Qy	19277	atagcttaagataaaaaggtatcatccag-ctttctgtgaacgtgcaatataagttaa	19333
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Qy	19338	aatgcacaaggtttctctgaaagccaaaccctgctcttaacaaaaatcataaaagttta	19395
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Qy	19396	aaaagatgctgtataaaaactccttatggtcacaacatagaanaaatggaataaatatgtcta	19455
Dd	4014	AAAAAGCTTATAAAAATCTTA-CTTATGTATCAAACTTTAAAAATTATGATTAATGTCTTA	4072

OY	19456	tgaggcttatataaataaagcttaacgttaaacacacacacataaagagtaaat	19515
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OY	19516	gcttactctgtaataaaatcatacaagaagtaatttaataataaattgylttagctt	19575
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OY	19576	tcttttgctctaaaaactataataaataggtcctaaaggaacaatcattctctagaga	19633
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OY	19636	tcatgaagattaaagactttaaaacaacttggcaattagaacagcatcaaccaagttgca	19695
Db	4253	TCTAATAAGTTTAAAACTTTAANAACAACTTTGGCAATTAGTAGCATTCACAAGATGCA	4312
OY	19696	atgccttggttgaatgtaataataatctcatctgcacattaaacaaagcagttglaty	19755
Db	4313	ATGCCTGGTTGGAAATGAAATTCATTCATCTGCACGTTAAACAAAGCAATTGTATG	4372
OY	19756	cttgtagacatgagccagagccagagccctcatctgtccccccttcaactaaagtgctcca	19815
Db	4373	CTTTGTCACATGGCAGGCGCAGAGGCCCTGATGTCTCCCTTCACATAAGATGCTTCCA	4432
OY	19816	gtccaccagagcggtggcgctgcagatgtaagtcctttccagagattccagagcttgaglaata	19875
Db	4433	GTCGGCCAGCGCTGGGCTGCACATGGTAGCTGTTTCCAGGATTCATACGCTTGATTAATA	4492
OY	19876	agtcatagcacaaactctctctgctat-----ccctgtggtgaagcccg	19919
Db	4493	AGTCATGCCAGGCTCTCTCTGCTATATCCCAAGCTGGTAACCTCGGGGTACGCCCTCG	4552
OY	19920	agggccatccagcctcgcgtctcccaacaactaagtctactc- atgtctctcaccagag	19978
Db	4553	AGGGCCATCCAGCCCTCGCTCTCCCAACACTAAGTTCACCTCTGTCTCTCACAGCAGGG	4612
OY	19979	aggaactatagatctccttga 20000	
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RESULT 4  
HSJ1112D6/c  
LOCUS HSJ1112D6 135305 bp DNA PRI 23-NOV-1999  
DEFINITION Human DNA sequence from clone 1112D6 on chromosome 6q21-22.2,  
complete sequence.  
ACCESSION AL080317  
VERSION AL080317.11 GI:5830430  
KEYWORDS HMG: Cpg Island.  
SOURCE human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 135305)  
AUTHORS Patel,R.  
TITLE Direct Submissions  
JOURNAL Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
COMMENT On Sep 6, 1999 this sequence version replaced gi:5791529.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP. Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence is  
the entire insert of clone 1112D6. This sequence has been finished





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Qy	19850	ccagaattctacagccttggagtaataagtcatagcacaactctctctgcta-----	19900
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QY	19900	ttccctgtagttagcccccgaagggatcttcagccctccgcgtctcccaactaagttcactt	19959
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QY	19960	catctctccacacagaagaacttagattagattccttctga	20000
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RESULT	5		
AC011036			
LOCUS	AC011036	137413 bp	DNA
DEFINITION	Homo sapiens clone 7_E_18, *** SEQUENCING IN PROGRESS ***	29-OCT-1999	HTG
ACCESSION	AC011036		
VERSION	AC011036.2	GI:6139104	
KEYWORDS	HTG; HTGS_PHASEL.		
SOURCE	human		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 137413)		
TITLE	Birren,B., Linton,L., Nusbaum,C. and Lander,E.		
JOURNAL	Homo sapiens, clone 7_E_18		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 137413)		
	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dekrellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kamp,L., Karatas,A., Klein,J., Lenczky,J., Lieu,C., Locke,K., Macdonald,P., Margulis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomasan,N., Stojanovic,N., Sudranthan,A., Talamas,J., Testlaye,S., Tyrrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Oct 29, 1999 this sequence version replaced gi:6002002. All repeats were identified using RepeatMasker: Smlt, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a> . * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
	1	2686: contig of 2686 bp in length	
	*	gap of unknown length	
	*	2687 10073: contig of 7387 bp in length	
	*	gap of unknown length	
	*	10074 18819: contig of 8746 bp in length	
	*	gap of unknown length	
	*	18820 31866: contig of 13047 bp in length	
	*	gap of unknown length	
	*	31867 56808: contig of 24942 bp in length	
	*	gap of unknown length	
	*	56809 90490: contig of 33682 bp in length	
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FEATURES		Location/Qualifiers	
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Db	58889	ATTCTTGCCCTGAATTAATTACTGCGTTGTTTTTTTAAAAAAATGTTTAACTAACT	58948
QY	18977	cagaaagttgacacgtgcaagaattatctgcgaagtcataga - aacgaegtata	19034
Db	58949	CAGAAAGTTGAGACATGTCGAAGAAATTTCTCTCGAAAGCTGTGAAGAAAAAGTTATA	59008
QY	19035	aaaaattatcacaanaaatalatgtrtaatttgaagaataaagaagcctctgtaactat	19094
Db	59009	AAAAATTTATGCAAAAAATGTTGTATAATTAAAAGTATAAAGCCTCTGTGACTATT	59068
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QY	19155	ttagaagaagcctataagaatggtgttcttaccatataaagtt - aaaaaattt	19213
Db	59129	CTATAGAGAGCATAGATGTGGATTTTCTTACCTCATTTAAAAAGTTAAAAAAATCATT	59188
QY	19214	gtcttgaaagtttaaagcaagtttaaalyttaatltgtanaaaaaaattctgtgttaa	19273
Db	59189	GTTTGAAGAGTTTATAGCAAGTTTAAAAAGTTAAATTTGT - AAAGAAATTTCTGTGTAA	59247
QY	19274	ctaattacctaagaataaaaggtatctcgaagtttctgtgaactggaacttaagta	19333
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Db	59308	AAAATGCACAGGTTTTTCTTAAACACCAACTCTCCTTTAACAAAAATTTAAAGGT	59367
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Db	59368	TAAAAAGGCTATATAAAATCTTA - CTTATGATCAACAACATTAAAAATTTGATATAATGTGC	59426
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QY	19574	ttctctgtgtcataaacaataaanaataggtcccaagaagaacattactactagag	19633
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QY	19634	gatacataagtttaaagacttaaaacaacttgygcaattaaagaacatatacaagaatgc	19693
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QY	19694	aaatgacctggttgaataatgatcatcaatatctcgtcacataataaacaagaagtggtta	19753
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QY	19814	caatccaccagcgtyggctgcattgtagctctttccagaagtttcaagccttgaagtaa	19873
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QY	19918	cgaagggcatcacagctcgtctctccacaacataagttcaattc - atgtctctccacagag	19976
Db	59907	TGAGGGCCATCAGAGCTCCGCTCTCCCAACACATAATTCACTTCGTTGTCTCTCAGACAG	59966
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[illegible]

Dh 16892 AATCTATCATGACCTTTCAG-TGAATGCTTAGAGTTGAGCCCTTAAGAGACA 16950  
Qy 17410 gaattgagcatcagagagctcggaattttagaagcctagctgcgattctccagctg 17469  
Dh 16951 GGAATTCCTACCTGGGGGAGCTACATATTTTAAGCAGTCTGGTACTACCTAGCTG 17010  
Qy 17470 attaaagcactccctacacatccggtgctcaggggtttgtcctgcgctacccg 17529  
Dh 17011 AATTAAGCC-CTTCCTTTACAACTCGGTATCTGAGAGCTTTATCAGCGGTCTCTG 17069  
Qy 17530 ctacattcttggttccctgaccgggaaagtgatlaacagatggtcgaagcgtc 17569  
Dh 17070 CTACATTCTTGTTCTCCCTGACCGGAAACATGATTAAGTACAGAGCGCGGAGCGCC 17129  
Qy 17590 cttagcgagcttagcctgcctctggaacatccctgctgggagctccaacagccag 17649  
Dh 17130 CTTAG-----GCCGCGCTGGGAGCATCCCTGCAGGGGACTCCGGCCAGCTGAG 17180  
Qy 17650 tgaagcgagctcgaagagctcctcgtggaagcattgccccgggtggagacacctgcag 17709  
Dh 17181 TGAGGC-AATCCAAAGAGCGCTCCCGGAAAGAAATTCCTGGGTGGAACGCTTAGCCAA 17239  
Qy 17710 agcagtggtgagcagcccccggtggaagatcaacagagtggtcgaacacgggaaagat 17769  
Dh 17240 AGCAGCGGTAGCAGGCGCCCTGCAAGAGATCAGCAGACTGGGTGAACACAGGAAGAAC 17299  
Qy 17770 tggcacttgagctcgaagacaaactatggtlaagactagctcttgaaactgcc-cac 17828  
Dh 17300 TGGACCTTGGGTGGAGCATCTGAACTTGTAAGTACTGTTGGAACCTTGGCACAC 17359  
Qy 17829 tccattgagagagagcagtcgcgtacacacagcggtgcttaagaac-ttggtt 17887  
Dh 17360 TCCACCTGAGTGAAGGCTGGCTCATACCCATGCTGTGCTGTATTAAGCCTTTGT 17419  
Qy 17888 ttggtttgacttggttgaacttacttgcagagagctgctctgggaacttcccactca 17947  
Dh 17420 CCGGTTTGAAGTGGCTG-----ACTGTGAAGCAGCTTTTGAAGCTG----- 17468  
Qy 17948 ttcccaactcaattgagtggaagcagtgctgctgacacacacaggtggtgctgtcc 18007  
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Qy 18008 ggcacttggtttgtttgactgactgactgactgactgactgactgactgactgactgact 18067  
Dh 17521 GGCACCTTTG-TCTGTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 17579  
Qy 18068 gacctgctgacttctgaactcactgacttctgacttctgacttctgacttctgacttct 18127  
Dh 17580 GATGTGCTTGATTTCTAGATTAAGTACTGATTTGTTGATTTGTTGTTGTTGTTGTTGTT 17639  
Qy 18128 gcaaaagtgtgctgctgcttcttaccgcttcttctgctgctgctgctgctgctgctg 18187  
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Qy 18188 agagtggttctgtctcgaagaaacatggttcagggcacaataaagccaccactcaga 18247  
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Dh 17940 TAAACCAAGGACCCAGACAGTTCGCTACATAGACAGTACAGCTGTTTGTAGACCA 17999

Qy 18482 ctgccccccacagtagttaaagagagcagaagaagagaaagaaacaggaacaaagaa 18541  
Dh 18000 CTCCCCGGCC-----CTACACTAGTTAAGACA 18030  
Qy 18542 agtcaagaagagagagagagagagagacagaagaatcaagaagagagagaaanaatag 18601  
Dh 18031 CAGCAGCATTAAGCGGCTGGCAGAGCAAGAAACCAAGCAGAGAGAAACGA----- 18084  
Qy 18602 agagaataatccaaagtagttaagaanaaatagtgctaccatctcccttaagaagcaag 18661  
Dh 18084 -GGCCATCTATCAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 18411  
Qy 18662 gtaatttaaaacctaattgataatlaaagytatctccgtaaccctgtaaacctta 18721  
Dh 18142 TAAATCTCAAACTTACA-----GGTTTCAGTAAAGTGAAGTTTGCTA 18187  
Qy 18722 ataccacttggttgaagtaaaagagcgatcccgaaagcactgagcgcttccat 18781  
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Dh 18487 AGGCTCTGTGACTACTGAGAAACAGTTATGTGCAAGTGTATTAAGTATTAAGTATTAAGTATTAAGTAT 18546  
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Dh 18726 GAACCTACATTAAGTAAAGTAAATGCAACAGCTTCTTTAAGCATCAACCTGCTCTTTA 18785  
Qy 19376 acaaaaatataaaggttlaaaagagctgttlaaaacttcccttactgtgtcaaacatgaa 19435  
Dh 18786 ACAAATAATTAAGGTTAAAGGTTAAAGAGCTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 18845  
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Dh 18903 TAAATTAAGTAAAGTAAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 18962

	QY	19556	taaaaaatggtttagctttcttggtcctaataactaaataatagtccttaaga	19615
	Dd	18963	TATATAAAGTGTATTAGCTTTCTTGGTGTTAAATAATATAAATAAGTGCTAAAGGA	19022
	OY	19616	acattcatttctactagagatcatagaagttaaagactaaaacaacttggcaattaa	19675
	Dd	19023	AATTTCATTTCCTAGAGGATCATAGAAGTTAAAGACTTAATAATGAACCTTGGCAATTAA	19082
	OY	19676	gaacagcatcccaagatgcataatgacctggtgttgaatygatccaatatctcatcgcaatt	19735
	Dd	19083	GACACATPCCACAGATGCATAAAGCCTTAGCTGAAATAGATCAATATATTCATCTGCACATT	19142
	OY	19736	aacaaaagaacattgttatgctctgtgcacatgagcagacagagcccctatctgccct	19785
	Dd	19143	AAACAANAACCAATTGTATTGCTTGTCGACATGATGATAGGCCAGAGGCCCTATTGTCCCCT	19200
	OY	19786	tccactaaagtgtgcctccatgcaccacaggcgtlgygctgatgtatgcctctttccagga	19855
	Dd	19203	TCCCGTAAAGTGTGCTCTCCAGTCGACCAAGTGTGGGCTCAGTGAGCTCTTTACAGAA	19262
	OY	19856	tctcacagctgagataaagaatcagtccaactcctctgct-----atccccg	19905
	Dd	19263	TTCTCAAGCTTGAGATTAATAGTCATGCCAACGCTCTCTGCTATNTCCAGAAATCCCTG	19322
	OY	19906	tgggtcagccccccgagggagccatccacgctcgcgtctccacaactaagtcttcatc	19965
	Dd	19323	CGGGTGTGCCCCCTGAGGGCCATTCACAGCTCTGTGTCCTCCCAACACTAAGTTCACCTTGTGC	19382
	OY	19966	tctcacacaagagagaaactaatgattcctctgga	20000
	Dd	19383	TCTCATGGCAGAGAGAGACTTACGATTTCTCTTGA	19417
RESULT	7			
ACOL1019				
LOCUS		ACOL1019	158463 bp	DNA HTG 30-NOV-1999
DEFINITION			Homo sapiens chromosome 8 clone RP11-90E12, *** SEQUENCING IN PROGRES	
ACCESSION			ACOL1019	
VERSION			ACOL1019.1	GI:6001969
KEYWORDS			HTG; HNGS_PHASEL.	
SOURCE			human.	
ORGANISM			Homo sapiens	
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;	
AUTHORS			Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 158463)	
			Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S., and Davis, R.W.	
JOURNAL			Unpublished	
REFERENCE			2 (bases 1 to 158463)	
AUTHORS			Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S., and Davis, R.W.	
TITLE			Direct Submission	
JOURNAL			Submitted (30-SEP-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	
COMMENT			----- Genome Center	
			Center: Stanford DNA Sequencing and Technology Development	
			Center code: SDSTDC	
			Web site: http://sequence-www.stanford.edu/group/human/	
			Contact: hum-info@sequence.stanford.edu	
			----- Project Information	
			Center project name: 680	
			Center clone name: RP11-90E12	
			----- Summary Statistics	
			Sequencing Vector: M13mp18, X02513	
			Chemistry: Dye primer; % of reads	
			Chemistry: Big Dye Terminator; 100% of reads	

[illegible]



[illegible]





[illegible]

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Db	199362	TGAAATATTTGGTGGAAAGTTTGAAAGAGAAAGTTATATAAAAAATTATTTCAAAA		199303
QY	19053	tatctataattctaaagtaataagacctccctgtagctacttgaagaacagctttagtg		19112
Db	199302	TGTTATATATTTTAAAGTATATAAAGCCTCCTAGTACTATTTTAAAAAAGTTATGTG		199243
QY	19113	caaggtgcataagaagaagtaaaatatactctttgtttaaagaattgaagaagcataaga		19172
Db	199242	CAAAATGTATAGAAAGAAATATAAATATACCTTTAGTATAAAAGATTATATAAGGCATAGAG		199183
QY	19173	atgtgattcttacctacattaaaggctttaaanaaattatgttttgaagtttaagcaa		19232
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QY	19233	gttttaaaatgttaattgtttaaanaaaatctctgtgtgtttaaactaatagctaaagataa		19292
Db	199122	GTTTTAAATGTTATATAT - TAAAGAAATCTGTGTGACACATTTAGCTAAAGTTAAA		199064
QY	19293	aaggtatacccaagttttctctgtgaactcgtgacataaagaataaaatgcacacaggttttc		19352
Db	199063	ACAGTATATCAGTATTTTCTGTGACTGACATTTAAAGTAAAAATGCACACAGTITTTTC		199004
QY	19353	ttgaagccaccaactgtccttttaaacaanaattataaaaggtttaaagaagctgttaaaa		19412
Db	199003	TTAAAGCATC - ACCGTGCTCTTTAACAAAAATTATAAAGGTTAAAAATAGCTATATAAT		198945
QY	19413	cttcacctatgttcaaacatgaanaatttgataaataatgctatagcttaggtttttaaat		19472
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Db	198884	TAAAGTTAATATTTAATAACACACTAATATATAAGGTAAATTTAGCTATCTGGATATAA		198825
QY	19533	atcacacaagaagtattataataataaagtgtttagcttcttggcttaaaact		19592
Db	198824	ATCATACAGAAACATATTATTAATATAAGGTTAGGTTACTCTTTATCTTAAACAC		198765
QY	19593	aataaaatagtgctcctaagaacatctactttactagagagatacagaagttaaagac		19652
Db	198764	ATATAAAAATTTGGCTCTAAGAGACGCTTACTTTACTAGAGGATCATATAAGTTAAGAG		198705
QY	19653	ttaaacaacaactcttggcaataaagacagcataccaagaatgcnaatgctgttgaatgy		19712
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QY	19713	atcaaatctccactcgtgacattaaacaaaagcgtgttagctctgtgacattgacag		19772
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QY	19773	ccagagggccctcatgttcccccctcacaataagtggtccctccagctccacagcgtyggc		19832
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QY	19833	tgcatgtgtagctctttcccaagattctacagcctgtgagataaagtcatagtccaaactctc		19892
Db	198524	TGCATGATAGCTCTTTTCCAGAGATTCTACAGTACAGTATTAAGTCATCCCAAGTTTCTC		198465
QY	19893	tcctgta-----tcctctgtgggttagcccccgaagggccatccagctctcgcttc		19942
Db	198464	TCTGTATATTTCTGAAGTCCTCTGAGGTCAGTCCCAAGGCCATCCAGCTTCATCTCC		198405
QY	19943	caacaactaagctcatcatgtctctcacaacagagaaggaacttagattctcttga		20000
Db	198404	CAACACATAGTTCACCTTCCCTAAGCACTTAGGAACACTA - AGACTTAGCAATTCCTTAGA		198349

ACCESSION	AC005406	
VERSION	AC005406.2	GI:4580403
KEYWORDS	HTG.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
	Eutharia; Primates; Catarrhini; Homiidae; Homo.	
REFERENCE	1 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
JOURNAL	Homo sapiens BAC Clone b128f11	
REFERENCE	2 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (08-AUG-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	3 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (10-SEP-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	4 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (23-SEP-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	5 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (01-OCT-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	6 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (04-OCT-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	7 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (14-OCT-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	8 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (05-NOV-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	9 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (11-NOV-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	10 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (21-NOV-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	11 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	
TITLE	Direct Submision	
JOURNAL	Submitted (26-NOV-1998) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
REFERENCE	12 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermld, H. and Roe, B. A.	

REFERENCE AUTHORS TITLE JOURNAL	Direct Submission Submitted (19-JAN-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA 13 (bases 1 to 226345)
REFERENCE AUTHORS TITLE JOURNAL	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A. Direct Submission Submitted (24-JAN-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA 14 (bases 1 to 226345)
REFERENCE AUTHORS TITLE JOURNAL	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A. Direct Submission Submitted (09-APR-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA 15 (bases 1 to 226345)
REFERENCE AUTHORS TITLE JOURNAL	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A. Direct Submission Submitted (22-APR-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA 16 (bases 1 to 226345)
REFERENCE AUTHORS TITLE JOURNAL	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A. Direct Submission Submitted (24-APR-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA 17 (bases 1 to 226345)
REFERENCE AUTHORS TITLE JOURNAL	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A. Direct Submission Submitted (12-OCT-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA On Apr 9, 1999 this sequence version replaced gi:3928116. Location/Qualifiers 1. 226345 /organism="Homo sapiens" /db_xref="taxon:9606"
COMMENT FEATURES source	
BASE COUNT ORIGIN	70721 a 47619 c 43447 g 64558 t

	Query Match	7.6%	Score 1517.8	DB 40	Length 226345
	Best Local Similarity	77.2%	Pred. No.1.2e-273		
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Db 222709	AGTCATACCTCTTAGGGAAGAGAGAACCCCTTCATATTGTTTATATTGTTTATAC	222768			
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QY 19694 aaatgccttggttgaatgatcaaatatcctatcgtcagatcaataaagaacagtgtta 19753
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QY 19754 tgccttgacatggcagcagcagcagcctatgttccccccttcacactaaagtgtctc 19813
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QY 19814 cagtcacacagcgttgaggctgcatgttagctctttccagagatctacagcctggagtaa 19873
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Db 225569 ACTTAGATCTCTTGA 225585

RESULT 10
AC004185 36921 bp DNA PRI 24-NOV-1998
LOCUS Homo sapiens clone UMGc:y14c094 from 6p21, complete sequence.
DEFINITION AC004185
VERSION AC004185.1 GI:3924650
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 36921)
AUTHORS Guillaudoux,T., Janer,M., Wong,G.K., Spies,T. and Geraghty,D.E.
TITLE The complete genomic sequence of 424,015 bp at the centromeric end
of the H1A class I region: gene content and polymorphism
Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9494-9499 (1998)
JOURNAL 98356185
MEDLINE Fred Hutchinson Cancer Research Center
REMARK The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 36921)
REFERENCE Geraghty,D.E. and Olson,M.V.
AUTHORS Direct Submission
TITLE Submitted (23-FEB-1998) Human Genome Center, University of
JOURNAL Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 36921)
REFERENCE Geraghty,D.E. and Olson,M.V.
AUTHORS Direct Submission
TITLE Submitted (24-NOV-1998) Human Genome Center, University of
JOURNAL Washington, Box 352145, Seattle, WA 98195, USA
COMMENT On Nov 24, 1998 this sequence version replaced gi:2905875.
overlapping sequences:
5': UMGc:y3c062
3': UMGc:y14c057

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Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 92.5%  
DS or two chemistry coverage: 100.0%  
Single stranded regions: 0

Sequence Validation:  
This sequence has been validated by multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below.  
Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

Map	Seq	Map	Seq	Map	Seq
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2844.34	2838.00	1091.71	1085.00	2387.38	2374.00
5171.90	5169.00	11619.04	11518.00	17878.57	17883.00
1127.00	1117.00	12730.55	12691.00	2714.05	2641.00
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8749.71	8563.00				
927.50	911.00				
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QY	17152	aaaccagagccctggcctgcctgcctacctaagctcgtgagcttaaatcgaacccctgacctag	17211					
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QY	17212	caactgttgttatctatagatccagacatgtatgaaaggaactgtatgaaagagacat	17271					
Db	33050	AACGGAGATTTATCTCTGTTTCCAGA-----CATTTGATGAAAGAAACAT	33094					
QY	17272	tgtgaatcctcgcgtctgtctgttctgttacctgtagccacggigtctcaacccctgtca	17331					
Db	33095	TGTGACACTCCCTGCGCTGCTGTTGTTGTTCTGTGACCAACAGTGATGACGCCCTGTCA	33154					
QY	17332	cgtacccctctgctctactcaatcgaatcagaacccctcattgcgaaccccttagagtgt	17391					
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QY	17392	gagcccttaaaaggagacgaagtgtgacatcagacagctcgtgattttgagacgtagcc	17451					
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Db	33393	GGACGCGCAAGGACACCCCTTGGGCGCTTAGAGCCTCGCTGTGGAGCATCCCTGCGGTG	33452					
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Oy	19166	catagaatgtggaattttaccatcataaaggittaanaaaatatgttttgaagtc	19225
Db	34749	CATAGAAATGTGGATTTTACCCTACATTAAAAAGGTTAAAAAATATTGTTTGAAGTG	34808
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Oy	19526	tataaaatctacagaagattatlaaatataaaatggtgtttagcttcttggtct	19585
Db	35108	TATAAATTCATACAGAGCATTTTATAATATAAAAGGTGTAGCTTCTTGGTCT	35167
Oy	19586	aaaaactataaaaatgagtccttaagaagaacatcatcttactagaagatcatagaag	19645
Db	35168	AAAACTATTAATAATAGATGCTTAAGGAAACATTTACTAGAGATCATGAAAGT	35227
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LOCUS	AC006047
DEFINITION	Homo sapiens clone UMGc:y14c057 from 6p21, complete sequence.
ACCESSION	AC006047



VERSION AC006047.1 GI:3924651  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 37139)  
AUTHORS Guillaudeau,T., Janer,M., Wong,G.K., Spies,T. and Geraghty,D.E.  
TITLE The complete genomic sequence of 424,015 bp at the centromeric end  
of the H1a class I region: gene content and polymorphism  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9494-9499 (1998)  
MEDLINE 98356185  
REMARK Fred Hutchinson Cancer Research Center  
The Clinical Research Division  
1100 Fairview Ave. N., P.O. Box 19024  
Seattle, WA 98109-1024  
2 (bases 1 to 37139)  
Geraghty,D.E. and Olson,M.V.  
DIRECT SUBMISSION  
Submitted (24-NOV-1998) Human Genome Center, University of  
Washington, Box 352145, Seattle, WA 98195, USA  
COMMENT Overlapping Sequences:  
5' : UMGC:Y14C094 (Genbank Accession: AC004185)  
3' : UMGC:Y24C027

Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
Genbank flat file format but are available as part  
of this entry's ASN.1 file.

Double stranded (DS) coverage: 79.7%  
DS or two chemistry coverage: 99.9%  
Single stranded regions: 2

Sequence Validation:  
This sequence has been validated by Multiple Complete Digest  
Mapping. Comparison of the experimentally derived map digest  
fragments with sequence-predicted fragments is given below.  
Small fragments below a variable cutoff (approximately 400-600bp)  
are not mapped and hence do not appear in the table. There are no  
significant remaining discrepancies between the experimental and  
predicted values. Uniquely ordered fragment groups are separated  
by dashed lines.

Map	Seq	Map	Seq	Map	Seq
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## FEATURES

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7.2% ; Score 1442.6 ; DB 40 ; Length 37139 ;



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QY	19586	aaaaactataaaaaatagtcctaaagaaatcttactttacttagagatcatgaagt	19645
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QY	19826	cgtggcgtgcatagtagctctttccagaattctacagcctgagfataaagtcacga	19885
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QY	19886	aactctcttgcta - -----tccctgtggctcagcccccgagggccatccagcctc	19935
Db	11716	AGCTCTCTCTGCTATATCCCGAAGTCTCTGTGTGGTCAGCCCCGAGGGCCATCCAGCTTC	11775
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Db	11836	TTGGA 11840	
RESULT 12			
AP000509			
LOCUS			
DEFINITION	AP000509 100000 bp DNA	PRI	28-SEP-1999
ACCESSION	Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,		
VERSION	AP000509		
KEYWORDS	AP000509.1 GI:5926696		
SOURCE	Homo sapiens DNA.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		

REFERENCE	Eutheria: Primates; Catarrhini; Homnidae; Homo.
AUTHORS	I (sites)
TITLE	Shima,S., Tamiya,G., Oka,A. and Inoko,H.
JOURNAL	Homo sapiens 2,229,818bp genomic DNA of 6p21.3 HLA class I region
REFERENCE	Published only in Database (1999) In press
AUTHORS	2 (bases 1 to 100000)
TITLE	Hirakawa,M., Yamaguchi,H., Imai,K. and Shlmada,J.
JOURNAL	Direct Submission
COMMENT	Submitted (21-SEP-1999) to the DDBJ/EMBL/GenBank databases. Miki Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases department; 5-3, Yonbancho, Chiyoda-Ku, Tokyo 102-0081, Japan (E-mail:m.kake@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470) This sequence is conducted by Tokai University as a JST sequencing Team. Principal Investigator: Hidetoshi Inoko Ph.D Phone:+81-463-93-1121, Fax:+81-463-94-8884, The sequence is submitted by Human Genome Sequencing in ALIS project of JST Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-Ku, Tokyo, 102-0081 Japan For further information about this sequences, please visit our sequence archive Web site ( <a href="http://www-alis.tokyo.jst.go.jp/HGS/top.html">http://www-alis.tokyo.jst.go.jp/HGS/top.html</a> ) or send email to webmaster@www-alis.tokyo.jst.go.jp.
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Oy 17097	-----aggaagaanaaagrgaataaagcgagatagccggcgcccttaggaaccagaccg 17151
Db 55353	TCTGTTTTAAAGAAAAAACAGAGAGCTAATAACCAAGACAGCAGCGCTTGCGCCAGGCCCA 55412
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Db 55413	AAACCAAGCCCTGGCGCTTCCCTTAACCAACAGTAGTTAAAACAACCAACCATGACTTAG 55472
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Oy	18398	aaatctatggaaccaaggttaacctgttaagccaagcacacagaccagcttctgtactgtaga	18457
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Oy	18518	aggaaagaacagagagcaaaaggaaaggtcaaaagagagagagagagagagagagacagaa	18577
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DEFINITION Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region
ACCESSION D84394
VERSION D84394.1 GI:2401262
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SOURCE Homo sapiens cell_line:CGM1 DNA, clone_1lb:T.Imai and M.V.Olson
clone:1109.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (sites)
AUTHORS Mizuki,N., Ando,H., Kimura,M., Ohno,S., Miyata,S., Yamazaki,M.,
Tashiro,H., Watanabe,K., Ono,A., Taguchi,S., Sugawara,C.,
Fukuzumi,Y., Okumura,K., Goto,K., Ishihara,M., Nakamura,S.,
Yonemoto,J., Kikuli,Y.Y., Shina,T., Chen,L., Ando,A., Ikemura,T.
and Inoko,H.
TITLE Nucleotide sequence analysis of the HLA class I region spanning the
237-kb segment around the HLA-B and -C genes
JOURNAL Genomics 42 (1), 55-66 (1997)
MEDLINE 97321045
REFERENCE 2 (bases 1 to 236822)
AUTHORS Mizuki,N., Ando,H., Kimura,M., Ohno,S., Miyata,S., Yamazaki,M.,
Tashiro,H., Watanabe,K., Ono,A., Taguchi,S., Sugawara,C.,
Fukuzumi,Y., Sato,M., Okumura,K., Goto,K., Ishihara,M., Kikuli,Y.,
Shina,T., Ando,A., Ikemura,T. and Inoko,H.
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TITLE Nucleotide sequence analysis of the HLA class I region spanning the
237 kb segment around the HLA-B and -C genes
JOURNAL Genomics 42 (1), 55-66 (1997)
REFERENCE 2 (bases 1 to 236822)
AUTHORS Mizuki,N., Ando,H., Kimura,M., Ohno,S., Miyata,S., Yamazaki,M.,
Tashiro,H., Watanabe,K., Ono,A., Taguchi,S., Sugawara,C.,
Fukuzumi,Y., Sato,M., Okumura,K., Goto,K., Ishihara,M., Kikuli,Y.,
Shina,T., Ando,A., Ikemura,T. and Inoko,H.
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Tashiro,H., Watanabe,K., Ono,A., Taguchi,S., Sugawara,C.,
Fukuzumi,Y., Sato,M., Okumura,K., Goto,K., Ishihara,M., Kikuli,Y.,
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VERSION	AL109912.4		
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	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 97906)		
AUTHORS	Slims,S		
TITLE	Direct Submission		
JOURNAL	Submitted (10-Sep-1999) Wellcome Trust Genome Campus, Hinxton,		
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:		
	humanequest@anger.ac.uk clone requests: clonerequest@anger.ac.uk		
COMMENT	On Sep 12, 1999 this sequence version replaced gi:5777438.		

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: djl114E20 Contig\_ID: 00340 acc-ALL09912 length: 64235 bp Unfinished: djl114E20 Contig\_ID: 00618 acc-ALL09912 length: 18869 bp Unfinished: djl114E20 Contig\_ID: 00679 acc-ALL09912 length: 13202 bp.

\* NOTE: This is a "working draft" sequence.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

FEATURES	Location/Qualifiers
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ORIGIN	

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Matches 2018;	Conservative	0;	Matches 424;	Indels 171;
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QY	17213	aatgttgttctatcatcccaactgtatgaaggcgatgtgtatgaaagaact	17272
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QY	18231	aagccacccctacttgaactatgttgaaaaaattccaagaagaaggtttaaaggagaattac	18290
Db	66338	AAGCCCAACCCCTATGGAACCTATGTGAAAAATTTCAAGAAAGAAATTTAAGGACATAT	66279

QY	17633	actccaacccagcaagctgacgcygacgtccgtacgaagctcctcctcyggtlaagcatttgcgcg	17692
Db	66917	ACTCCGAGCAGCCTGAGTGC	66859
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Db	66678	GTAATGGCACTTTGTCTGTGTTTGACTTGGCTTG---ACTTGGTAGGACTAGTCTTT	66623
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QY	17991	caaggtgtgctgtctccggcactttgtgttttggacttgactgaatgacttgat	18050
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Db	66456	TTGGTTTGGTGTAACTGGAAGTGTGTGTGCCCCCTTTTAAGTGTCTTTGTTTGT	66399
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Db	66398	GGTGTGTGTGTGTGTGACCGTGTGTTTGTCTCAAGAAACATGAGGCCACGACCAAT	66339
QY	18231	aagccacccctactgaactatgtttgaaaaattccaagaagagatttaaggaagatcac	18290
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Qy 19610 aaggaacatcattacttagagatcataga 19642
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```

## RESULT 15

## HS454G6

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

HS454G6 79376 bp DNA PRI 23-NOV-1999  
Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains  
trabecular mesenchymal inducible glucocorticoid response protein,  
TIGR, myocillin, ESTs and STS.  
298750.1 GI:2887277  
1q24; myocillin; TIGR.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 79376)  
Deadman, R.  
Direct Submission  
Submitted (27-OCT-1997) Chromosome 1 Project Group  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Feb 14, 1998 this sequence version replaced gi:2463060.  
IMPORTANT: This sequence is not the entire insert of clone 454G6.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we arrange for a small overlap between  
neighbouring submissions.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variations annotated may not be found in the sequence submission  
corresponding to the overlapping clone as we submit sequences with  
only a small overlap as described above.  
This sequence was generated from part of bacterial clone contigs of  
human chromosome 1, constructed by the Sanger Centre chromosome 1  
mapping group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1/  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The true left end of clone 454G6 is at 1 in this sequence. The true  
left end of clone 560B9 is at 79273.  
454G6 is from the library RPc13 constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong.  
For further details see http://Daapac.med.buffalo.edu/  
Location/Qualifiers

## FEATURES

## Source

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/map="1q24"
/clone="RP3-454G6"

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F12081 AA046699; match: F02925 AA131540 W06534 R36066  
AA13383; match: AA163561 F02925 AA131540 W06534 R36066;  
match: AA13383 AA163561 N89173 AA174814 AA057059; match:  
AA329084 W47082 AA043955 AA341783 AA353681; match:  
AA046487 AA369741 H08313 AA186895 H32730; match: H08333  
H08236 N42052 D61944 R27102 N32553; match: N30431 AA307150  
AA192"  
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repeat\_region 7933. .9328  
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22531. .22839  
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misc\_feature complement(23652. .24072)  
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repeat\_region 24008. .24290  
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repeat\_region 25895. .26364  
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repeat\_region 26397. .26697  
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repeat\_region 34725. .34904  
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repeat\_region 38382. .38682  
/note="Alusx repeat: matches 1. .302 of consensus"  
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/note="Alub repeat: matches 3. .296 of consensus"  
repeat\_region 39418. .39773  
/note="THE1A repeat: matches 354. .2 of consensus"  
repeat\_region 39775. .40120  
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/Note="Alusq repeat: matches 21..303 of consensus:
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Best Local Similarity 74.2%; Pred. No. 2.8e-248;
Matches 222; Conservative 0; Mismatches 477; Indels 294; Gaps 26;

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Db 10906 TGAAGGAGAGAGAGACCTTCTCATATGTTTATATCAGGCTGTTTAAAGAAAAA 10965
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Oy 17098 ggaagaagaagtgaataaagagcagatagcccgcgctctgagaaaccgacccaaga 17157
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Oy 17158 ggcctggcctgcctgcacatgaagctcgtagttaaatcgacccctgacctagacac 17217
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Db 11607 ACAAGTGGCTGAACACACAGAGAAAGAACTGGACATTCGAACTCAACATCTGAAATTTAG 11666
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Oy 17802 taagactgcttcggaacttg-cccactcacttgagtggaagatgagcctgcacaccc 17860
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11667 TAAAGATGATGTTTAAAGACTTGCCTCACTCCATCTGAGTGAAGAGGTGGCTCGATCACCC 11726
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 17861 acggcgctgcttatacagacacttggtttgtgtttgacttggttgaaattacttgacag 17920
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11727 AGGGTGTGCTGCAATGTGCATTTTGTTC----- 11756
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 17921 actgtctcttggaacttgcccaatccatcccaactcccaacttgagtggaagatgagcctga 17980
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11756 ----- 11756
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 17981 tctgataccacaggtgtgcctgtctcgcgcaacttgcttttcttgacttgacttag 18040
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 11756 ----- 11756
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 18041 attgcttaacatttggttttggttttgacatgctgctgattctcgaactcgaattc 18100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11775 ATTGCTGACACTTGTGTTTATGTTTATGTTTACTGTGCTGAATTTTGGTACACGATTTT 11834
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 18101 ggttcttctggttttggttgtaaacctgcaaaagtggtgtgctgaccttttaccg 18157
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Db 11835 GAATTCCTGATTTGTTGGTGTATTAACAGTAAAGTGTGGGTGTGCTCTTAAACCG 11894
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Oy 18158 ttcttctgttttggtt--gtgcatgtgtgtgagagtggtttgtgtcga-----ga 18210
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Db 11895 TTCTTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 11954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 18211 aacatggttcagagcaaaa-taagcccaactactagaacatgttgaaaaatttcaag 18269
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Db 11955 AAAATAGGTCAAGGTCAAAAGTAAGCCCACTGGAGACTGTATTAAGAAATTTCAAG 12014
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Oy 18270 aaagatttaaggagagatcaggtgttactatgacacatagaaaaaacttaagaacttggt 18329
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Db 12015 AAAAGATTTTAAAGGAGACTATGAGTCACTATGACTCCAGAAAACTTAGGACTTGTGT 12074
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Oy 18330 aaatagactggcacaacatagaggttggttggttgccatagaagaagagcctagacaggtcc 18389
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Db 12075 GNCATAGACTGCGCGCATTTAGAGGTGGTTGGCCATAGAAAGAAAGCTTAGACAGTTC 12134
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Oy 18390 ctgtttcaaatgtatgacacaaagtaaacctgttaagccaaagcacacagacacgttctg 18449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12135 TTTGTTTAAAGATATGACACAAAGTAACTGTAACTGTAAGCAAGCAGACCAATTTCCG 12194
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Oy 18450 taagtagacaattacagctgtttttagacccctcgcgcacacagtgattgaagagagc 18509
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Db 12195 TACATAGACAGTATACAGCTGTGTTTGAACCCCTTCCCTCCACAGTGTATTAAGGAACA 12254
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Oy 18510 agaaagagaggaagaaagagagagagagagagagagagagagagagagagagagagag 18569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12255 GCAGCATTAAGCGGCTGCGAGAGGCAAGAAAGACCAAGCAGAGAAAGAAAGAG----- 12307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 18570 agacagaagtaacaaagagaaagaaataagagaaataccaagtagtaagaanaaa 18629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12307 -----ACCATCTATACCAATCTTAAGTAAATTAACATAA 12341
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Oy 18630 aatagtacacctattccctttaaagccaaggttaatttaaactaaattgttaatt 18689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12342 ACAAG--GTCTTATTAATACCAAAAGATTAATGAATCCCAAACTTCAAGGTTTCAA 12398
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Oy 18690 aaagttatctccgttaacccctgttaacactccaataccacttggtgttagtgtaacaag 18749
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Db 12399 CAAAGTGAAGTTTGTCTAAAGTTAACAGTGAACATGTATATGTATGTACTTAATCTTG 12458
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Oy 18750 ggcgtatccggaagacactgagcccttcctacaaaaatcccttaaccagtaaccagcg 18809
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Db 12459 -----TAGCCTTAGACAGTACTAGTCCAAACATTAAGAAAGT----- 12497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 18810 atgcccagatgactatcatctgtagcagcgctgtcttgtaacaggaagaaaaa 18869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12497 -----TTGCTTTAAAAAAAAGAAATTAATTTCTTCA-----AAAAATTAAGAG 12543
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Oy 18870 aaagacgtgttggaaggaacaaattatgttaaagaagtgatatagtgtaaaattctgtct 18929
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12544 AAAAAGAGGGGGGAGCAGATTTATGT--AAAGAGGTATATAGTAAATTTCTTGTCC 12601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 18930 tgaataataataacgtg-ttgtttaagaagaagaataattgttaataagtcagaagaattgag 18988
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12602 TGAATTAATTAATACGCTTGTTTAAAGAAAAAACTTTGTAATTAAGTCAAAAATTTAG 12661
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 18989 aacatgcaagaatatacttgagaaaggtacatagaagaagatgtata-aaaaattatgca 19047
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Db 12662 ACATGTTAAAAAATTTGTGTGCGAAAGTGTGTAAGAAAAAAATGTTATATAAATTTATGCA 12721
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Oy 19048 aaaaatattgataaatttgaaagtaagagcctcctcgtgact-attgaaagaacagtt 19106
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 12722 AAAAATGTTATTAATTTAAAGCTTAATAGCCTCCTGACTACTGTTTAAAAAACAGTT 12781  
QY 19107 tatgtcaagtgatcataagaagaatataatatttggtaaaagattagaagagc 19166  
Db 12782 TATGTCAAGAGTATATAGAAAGTAAGTACCTTACTAGTAAAAAGATTATAAGGGC 12841  
QY 19167 atagaatgtgactttaccatcataaagggttaaaaaattatctgttgaagttc 19226  
Db 12842 ATAAAAACGTGGATTTTACTACATTAAGTTAAAAAATATGTTT----- 12893  
QY 19227 aagcaagtttaaatgttaaatgttaaaaaaatctgtgttaaaactaattagctaa 19286  
Db 12893 --AAAAGTTTAAACCTTAATGT- AAGAAAAATTTGTGTGAACATATTAGCTAAA 12949  
QY 19287 gataaaaaggatcatccagttttctgtgactgagacatlaaagtaaaaatgcaacag 19346  
Db 12950 GTTAAAAAGTATCATCCATTTTCTGTGACTAGACATTAAGTAAAAATGCAACAG 13009  
QY 19347 ttttcttgaagcaacacctgctctttaaacaanaattataaagggtlaaaaaggtctg 19406  
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QY 19407 taaaaactaaccttatggtgcaacaagaanaattggaataatgtctatgagtttat 19466  
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QY 19467 taaaatlaagtttaacataataacacacataataaagtaaaatttagcttatctgct 19526  
Db 13130 TAAATTAAGTTTAACATTAAATACACCCATATATAAAGTAAATTTAATCTAGCTGT 13189  
QY 19527 ataaaaatcatacaagaagatatataataaataaagtggtttagcttcttgtctta 19586  
Db 13190 ATAAAAATCATACAGACAGCATTTATTAATATTAATATGTTAATCTTTGTCCTA 13249  
QY 19587 aaactaat-aaaaataggtccctaagaagaacttactactaaggtacataagaatc 19645  
Db 13250 AAAACTTAATAAAAATAGATGTAAGAAACATCTATTTACTAGAGATCATAGAAAT 13309  
QY 19646 taaagacttaaaacaactttggaattaaagaagcatlaccaagatccaatgcctgtt 19705  
Db 13310 TAAAGACTTAAACAAACTTTGGCAATTAGAGGGCATACCAAGATGCAATGCTGT 13369  
QY 19706 gaaatgatacaatattccatctgcacattaaacaagaagtggtatgtctgtgcaca 19765  
Db 13370 GAATATGATCAAAATATTCATTCGACGTTATA-AAAAGCAATGTATGCTGTGCACA 13428  
QY 19766 tggcagggccagagggccctcatgtccccccttcaactaaagtggtccctcagttcacagg 19825  
Db 13429 TGGCAGGCCAGAGGCCCGCATTTGCCCTTCCACTAAGTGCTCCAGTCCACACAGG 13488  
QY 19826 cgttggcctgcatgtgactcttccagagatctacagacctgagtaataagtcatagcca 19885  
Db 13489 CGTGGCTGATGTAGTCTTTCCAGAGTCTACAGCCTAGATTAAGTATGATGCCA 13548  
QY 19886 aactcctctgtcfa-----ttccctgttggtcagccccgagggccatccagctc 19935  
Db 13549 AGCTCTCTGCTATATCCGAAAGTCCCTGTCAGGTCAAGCCCAAGGCCATCCAGCTTC 13608  
QY 19936 cgtctccacaactaagttactactatgtctccacacagagagaaactta 19988  
Db 13609 CGTCTCCCAACATAAGTTCACTTGTGTCTCATGCGCAGGAGGAGACTTA 13661

Search completed: February 29, 2000, 08:44:14  
Job time: 77325 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2000, 20:12:08 : Search time 21727.1 Seconds  
(without alignments)  
-3493.772 Million cell updates/sec

Title: US-09-339-352-8\_COPY\_1\_25000  
Perfect score: 25000  
Sequence: 1 aggaaccttcgaagaggaac.....cttcaccttgcaatacca 25000

Scoring table: IDENTITY\_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:\*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb\_bal:\*  
2: gb\_bal:\*  
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47: gb\_bal:\*  
48: gb\_bal:\*  
49: gb\_bal:\*

50: gb\_P13:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	25000	100.0	102258	11 HS295C6	297876 Human DNA s
2	1700.4	6.8	78661	11 AC005350	AC005350 Homo sapi
3	1675.4	6.7	149566	11 AC003081	AC003081 Human BAC
4	1670.2	6.7	212118	44 AC009264	AC009264 Homo sapi
5	1659.8	6.6	152794	44 AC009794	AC009794 Homo sapi
6	1592.6	6.4	192151	33 AC007282	AC007282 Homo sapi
7	1574.8	6.3	220218	40 AC006288	AC006288 Homo sapi
8	1563	6.3	94320	10 AC002564	AC002564 Human BAC
9	1558.6	6.2	73029	11 HSBA329J7	AL118497 Human DNA
10	1548.2	6.2	161326	11 AC004067	AC004067 Homo sapi
11	1546.2	6.2	110401	11 AC004068	AC004068 Homo sapi
12	1541	6.2	181883	44 AC016735	AL080275 Homo sapi
13	1533.2	6.1	118205	32 HSDJ149L1	AL022401 Homo sapi
14	1528.4	6.1	206784	11 HS93L7	AC015692 Homo sapi
15	1524.2	6.1	144159	43 AC015692	AC015692 Homo sapi
16	1521.4	6.1	151834	40 AC005399	AC005399 Homo sapi
17	1519.6	6.1	184490	10 HS082828	U82828 Homo sapi
18	1519.2	6.1	163712	11 AC004065	AC004065 Homo sapi
19	1517.6	6.1	292721	40 AF130343	AF130343 Homo sapi
20	1515.8	6.1	182865	43 AC011330	AC011330 Homo sapi
21	1514.4	6.1	126149	40 AC006352	AC006352 Homo sapi
22	1514	6.1	119580	10 AP000466	AP000466 Homo sapi
23	1512.8	6.1	117954	10 HSAC02065	AC002065 Human BAC
24	1511.4	6.0	148800	33 AC007028	AC007028 Homo sapi
25	1511.2	6.0	167171	33 AC006269	AC006269 Homo sapi
26	1508.4	6.0	166219	11 AC003084	AC003084 Human BAC
27	1507.6	6.0	186324	41 AC009405	AC009405 Homo sapi
28	1507.4	6.0	152393	41 AC010682	AC010682 Homo sapi
29	1502.4	6.0	156929	41 AC009277	AC009277 Homo sapi
30	1501.6	6.0	181751	42 AC008784	AC008784 Homo sapi
31	1500	6.0	143119	42 AC011059	AC011059 Homo sapi
32	1499.4	6.0	140167	11 AC004010	AC004010 Human BAC
33	1497.4	6.0	170208	32 CNS01DUA	AL133323 Homo sapi
34	1496.4	6.0	170967	40 AC005023	AC005023 Homo sapi
35	1495.6	6.0	143427	10 AC002432	AC002432 Human BAC
36	1494.2	6.0	136968	32 HS668J24	AL033436 Homo sapi
37	1493.6	6.0	141773	32 HS1007G16	AL121980 Homo sapi
38	1492.6	6.0	194000	33 AC000016	AC000016 Homo sapi
39	1492.6	6.0	128000	33 AC004046	AC004046 Homo sapi
40	1487.4	5.9	98770	11 HS364I11	AL031319 Human DNA
41	1486.8	5.9	125290	40 AC004986	AC004986 Homo sapi
42	1484.4	5.9	192548	40 AC005296	AC005296 Homo sapi
43	1483	5.9	175463	43 AC007272	AC007272 Homo sapi
44	1482.4	5.9	198363	44 AC013545	AC013545 Homo sapi
45	1482.2	5.9	172383	45 AC008065	AC008065 Homo sapi

# ALIGNMENTS

RESULT 1  
HS295C6  
LOCUS HS295C6 102258 bp DNA  
DEFINITION Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains  
ESTs, CA repeat, STR and Cpg island.  
ACCESSION 297876  
VERSION 297876.1 GI:2582745  
KEYWORDS 1q24; Cpg island; repeat polymorphism.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 102258)  
AUTHORS Grafham,D.  
TITLE Direct Submission  
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Nov 2, 1997 this sequence version replaced g1:2465042.  
IMPORTANT: This sequence is the entire insert of clone 295C6.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variations annotated may not be found in the sequence submission  
corresponding to the overlapping clone as we submit sequences with  
only a small overlap as described above.  
This sequence was generated from part of bacterial clone configs of  
human chromosome 1, constructed by the Sanger Centre chromosome 1  
mapping group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1/  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The true left end of clone 295C6 is at 1 in this sequence. The true  
right end of clone 295C6 is at 102258.  
295C6 is from the library RPC11 constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong.  
For further details see http://bacpac.med.buffalo.edu/  
Location/Qualifiers  
1. .102258  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/map="1q24"  
/clone="RP1-295C6"  
/clone\_lib="RPC1-1"  
891. .1180  
/note="AluSq repeat: matches 298. .9 of consensus"  
1375. .1683  
/note="AluSP repeat: matches 303. .1 of consensus"  
2028. .2310  
/note="AluSq repeat: matches 300. .1 of consensus"  
2612. .2903  
/note="AluSq repeat: matches 301. .1 of consensus"  
complement(4475. .4866)  
/note="match: 223618 SIS containing (CA) repeat"  
4625. .4670  
/note="23 copies of GT 100 & conserved; differs from  
223618"  
4766. .4897  
/note="MIR2 repeat: matches 145. .1 of consensus"  
4969. .5140  
/note="MER42c repeat: matches 1475. .1300 of consensus"  
5146. .5448  
/note="AluJo repeat: matches 302. .1 of consensus"  
5503. .5795  
/note="AluSq repeat: matches 1. .299 of consensus"  
5797. .3525  
/note="MER42c repeat: matches 1265. .1124 of consensus"  
5923. .6039  
/note="LIMB6 repeat: matches 920. .804 of consensus"  
6123. .6415  
/note="AluX repeat: matches 1. .292 of consensus"  
7799. .8099  
/note="AluX repeat: matches 302. .1 of consensus"  
9002. .9302  
/note="AluSP repeat: matches 2. .303 of consensus"  
9692. .9983  
/note="AluJo repeat: matches 1. .301 of consensus"  
10986. .11071  
/note="MIR2 repeat: matches 146. .60 of consensus"

repeat\_region 11583. .11766  
/note="MIR repeat: matches 262. .70 of consensus"  
repeat\_region 12180. .12479  
/note="AluSq repeat: matches 1. .300 of consensus"  
repeat\_region 13246. .13500  
/note="MIR repeat: matches 256. .1 of consensus"  
repeat\_region 13907. .13973  
/note="MIR repeat: matches 75. .141 of consensus"  
repeat\_region 13975. .14489  
/note="MIR repeat: matches 526. .1 of consensus"  
repeat\_region 15702. .16064  
/note="MIR repeat: matches 1. .371 of consensus"  
repeat\_region 16144. .16585  
/note="MIR repeat: matches 9. .466 of consensus"  
repeat\_region 17173. .17534  
/note="MIR repeat: matches 105. .449 of consensus"  
prim\_transcript <17786. .>18427  
/note="match: multiple ESTs; match: AA165668 C16515  
AA077391"  
repeat\_region 18004. .18120  
/note="3 copies of 39 mer 81 & conserved"  
prim\_transcript 19377. .>21532  
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T62974 AA283144; match: T57835 F00049 N75628 AA382351  
AA300207; match: W57181 N52820 AA337499 W87891 H84729;  
similar to endogenous retrovirus POL POLYPROTEIN"  
prim\_transcript <22156. .>22928  
/note="match: multiple ESTs; match: AA401243 AA258918  
AA248892 AA096209 R36280"  
repeat\_region 23025. .23060  
/note="3 copies of 12 mer 94 & conserved"  
repeat\_region 23519. .23865  
/note="MIR2 repeat: matches 105. .449 of consensus"  
repeat\_region 24473. .24785  
/note="AluSq repeat: matches 1. .299 of consensus"  
repeat\_region 25027. .25058  
/note="16 copies of 2 mer 88 & conserved"  
repeat\_region 25877. .25987  
/note="LIPAS repeat: matches 788. .892 of consensus"  
repeat\_region 26022. .26312  
/note="AluSP repeat: matches 1. .295 of consensus"  
repeat\_region 26752. .27050  
/note="AluSq repeat: matches 1. .299 of consensus"  
repeat\_region 28012. .28312  
/note="AluSq repeat: matches 1. .303 of consensus"  
repeat\_region 28316. .29066  
/note="LIMB3 repeat: matches 109. .907 of consensus"  
repeat\_region 29517. .29629  
/note="MIR repeat: matches 262. .151 of consensus"  
repeat\_region 29631. .29928  
/note="Alu repeat: matches 1. .295 of consensus"  
repeat\_region 29937. .30237  
/note="AluSq repeat: matches 1. .301 of consensus"  
repeat\_region 30238. .30315  
/note="MIR repeat: matches 158. .76 of consensus"  
repeat\_region 31096. .31287  
/note="MIR repeat: matches 56. .262 of consensus"  
repeat\_region 31289. .31379  
/note="MIR2 repeat: matches 146. .56 of consensus"  
repeat\_region 31479. .31525  
/note="MIR2 repeat: matches 146. .95 of consensus"  
repeat\_region 33069. .33318  
/note="MIR repeat: matches 9. .253 of consensus"  
repeat\_region 35565. .35744  
/note="MIR repeat: matches 262. .74 of consensus"  
repeat\_region 36165. .36466  
/note="AluX repeat: matches 1. .302 of consensus"  
repeat\_region 36692. .36944  
/note="MIR repeat: matches 3. .240 of consensus"  
repeat\_region 36999. .37299  
/note="AluX repeat: matches 301. .1 of consensus"  
repeat\_region 37924. .38114  
/note="LIMB2 repeat: matches 1055. .866 of consensus"

repeat_region	38108..38475	note="MST1 repeat: matches 426..1 of consensus"
repeat_region	38479..38657	note="L1M2 repeat: matches 874..687 of consensus"
repeat_region	38658..38957	note="AluSg repeat: matches 300..1 of consensus"
repeat_region	38958..39580	note="L1M3 repeat: matches 699..85 of consensus"
repeat_region	39581..39875	note="AluSg repeat: matches 292..1 of consensus"
repeat_region	39877..39951	note="L1M4 repeat: matches 88..14 of consensus"
repeat_region	39944..40919	note="L1 repeat: matches 4416..5390 of consensus"
repeat_region	40769..41662	note="L1P2 repeat: matches 1..893 of consensus"
repeat_region	41764..42556	note="L1 repeat: matches 5133..4305 of consensus"
repeat_region	42557..42857	note="AluY repeat: matches 1..301 of consensus"
repeat_region	42876..43925	note="L1 repeat: matches 4313..3215 of consensus"
repeat_region	44235..44498	note="MER43 repeat: matches 3..272 of consensus"
repeat_region	44788..44860	note="MIR repeat: matches 154..82 of consensus"
repeat_region	44933..45220	note="AluSg repeat: matches 289..2 of consensus"
repeat_region	45304..45336	note="AluY repeat: matches 1..301 of consensus"
repeat_region	45337..45637	note="AluY repeat: matches 1..301 of consensus"
repeat_region	45934..46220	note="AluY repeat: matches 302..14 of consensus"
repeat_region	46817..46935	note="MIR repeat: matches 35..154 of consensus"
repeat_region	47393..47577	note="AluSg repeat: matches 1..302 of consensus"
repeat_region	48309..48404	note="MIR repeat: matches 48..140 of consensus"
repeat_region	48620..48862	note="MIR repeat: matches 347..102 of consensus"
repeat_region	48865..49159	note="AluSg repeat: matches 1..296 of consensus"
repeat_region	51182..51467	

Query Match	Best Local Similarity	Matches 25000	Conservative	100.0%	Score 25000	DB 11	Length 102258
Qy	1	aggacctcttcaggagagactacaacccactggtcccaagaaqtaaaagagacacaca	60				
Db	39961	AGGACCTTTCAAGSAGAACTACAACCCACGCTCTCAAGAGTAAAGAGACCAACA	40020				
Qy	61	aatggaagaacatccatcgcattgcatgtaggaaaaaatcaatataatgaatgycat	120				
Db	40021	AATGGAAAGACATTCGCATGCTCATGATGATGAAAAATCAATATCATGAAAAATG	40080				
Qy	121	tgctccaagtgattatgatagctcatgcatcccccacatcaagctcccatgacttct	180				
Db	40081	TGCTCAAGGTATTTATATGATTCATGCGACATCCCATCAACCTACATGACTTTCTT	40140				
Qy	181	cagaattgaaaaatactacttaagtatcatatgaaacccaaaaaagacgtcgtatg	240				
Db	40141	CAGAAITTGAAAAATCTACTTTAAAGTTCAATATGGAACCAAAAAAGACCTCGCAT	40200				
Qy	241	agataatccctaagcaaaaaaagaacaagcttggaggtcatcatgtcactgacttca	300				
Db	40201	AGATATCTCTAAGCAAAAAGAACAAAGCTGGAGCATCATCTACTGACTTCAACTAT	40260				
Qy	301	actacaagctacagtaaccacaaaacagcatgtgtactgtgtaccacaaacagaat	360				
Db	40261	ACTCAAGGCTACAGTAACTCAAAACAGCATGTCTGTTACCAAAACAGAAATTAA	40320				

QY	361	aatggaatggaacacatccctcagaataaataccacacacatcacaacatcgaactcttg	420
Db	40321	AATGGAAATGGAACAGTCCCTTAGAAATATACCAACATCTACAAACCATCTGATCTTTG	40380
QY	421	acaaaccttaaaagaacaaataatagggaaagatctccattataatgctgctgg	480
Db	40381	ACAAACCTTAAAGACAAAGAAATAGGGAAAGATTCCTATTATATAATGTGCTGGG	40440
QY	481	aaaactgctagccatgtagaaagctgaaactgaaactgaaactccctccactataca	540
Db	40441	AAAACGGCTACCCATATATTATAAAGCTGAAACTGGATCCCTTCCTCCACTTATACA	40500
QY	541	aaatthaattcaagatggatataaagactaaatggttaagacctaaacccataaacctcg	600
Db	40501	AAATTAATTCAGATGGATTAAAGCTTTAAAGCTTTAAAGCTTAAACCATTAAGCCCTAG	40560
QY	601	aagaaacctaggcaataccatccagtaacatggaatgggcaaggacatcatgactgaaac	660
Db	40561	AAGAAACCTTAGGCATTAACATTCAGTACATAGCATGGGCAAGGACTTCATGATGAAC	40620
QY	661	accaaagcaatgycacaacaaacccaatgycacaacaggatccaatlaaactaagag	720
Db	40621	ACCAAAAGCAATGGGACACAAAACCAAAATTACAAACGGATCCAAATTAACCTAAGAG	40680
QY	721	ctctggaacagaaagaataatcatcagaagtgaacaggcatccatagaatgggagaaat	780
Db	40681	CTTCTGACACGAAAGAAATATATAGATGACAGCATCTTACAGATGGGAGAAAT	40740
QY	781	tttcaaatctacccatctgacaagaaggctaaatccagaatctacaagaactaaaca	840
Db	40741	TTTTCAATCTCCCATCTGACAAAGGGCTATATCCGAATCTCAAGAACTTAACA	40800
QY	841	aatttgcagaagaaaaatctaaacaaaccccatcaaaaagtgggcaagatatgacagac	900
Db	40801	AATTTGCAAGAAAAAATCAAAACCCCATTAAGGGGCAAGGATATGAACAGAC	40860
QY	901	actctcacaagaagacatttlatgacccaacagacagatgaaaaatgltcatcatcac	960
Db	40861	ACTTTCAAAAAGACATTTATGACGACCAAGACAGTGAATAAAGTTTCATCATCAC	40920
QY	961	tggccatcaggaacatgcaaatccaacacacaaatgaatataccattccacaacagttaga	1020
Db	40921	TGGCCATCGAAGACATGCAAAATCAAAACCCACATAGATACCATCTCACACAGTTAGA	40980
QY	1021	tggcaatcatataaagtcaagaaacacacagctgcctggagagatgctggagaataggaa	1080
Db	40981	TGGCAATCATTTAAAGTCAAGAACACAGGTGCTGGAGAGAGTGTGAGAAATAGGA	41040
QY	1081	caatttacaactgtgtgtyggagctgtaaaactgltcaaacattgtggaagacagtgtgc	1140
Db	41041	CACTTTACACTGTGTGGGTGACTGTAACTGTGTCAACCATTTGGGAAGACAGTGTGC	41100
QY	1141	gattctcaagagatctagaactcagaataatctatggaaccagccaatcccatctcgggta	1200
Db	41101	GATTCTCAGAGATCTAGACACTAGAAATATCTTTTGACCCACACCATCCCATACGGGTA	41160
QY	1201	gtlaccaaaaggattataatcayctgcgtataaagaacatgcaatgcatgltatgttattg	1260
Db	41161	TGTACCCAAAGATTATTAATATCTGCTATTAAAGACACATGCAACATGATGTTATTG	41220
QY	1261	tggacatctacaaatagaaagacctggaacaaacccaatgctcatcagtgtagact	1320
Db	41221	TGGCATATTCCAATAGCAAAAGACCTGGAACCAACCCAAAGTCTCATGAGTGAAGCT	41280
QY	1321	ggattaagaanaatgycatgltatacacagtygaaatattatgycaccaataaaaggatga	1380
Db	41281	GGATTAAAGAAATGGGCATGATACACAGTGGATATTATTCACACCCATTAAGAAAGATGA	41340
QY	1381	gttcaactccttttgtaggaacttgatgaagtgtgaaacacatcatcttgagaaactctc	1440
Db	41341	GTTTCAAGTCTTTTGAAGGACATGATGAAGTTGGAAACCATCATCTTGAGCAAACTATC	41400
QY	1441	acaagagatgaacccaacacacacatglttcacatcaatggttggaaattgaaacatgag	1500



Db	41401	ACAAAGATTAAGAAACCAACACACATGTTCTCACCTACATAGGTGGAAATGAAACATGAG	41460
Qy	1501	aacacctiagacacaggtgtggtggaacatacacacacagggccgtctgtggtcgtggtggtgga	1560
Db	41461	AACACTTAGACACAGGGTGGGGAACATCACACACAGGGCCCTGTGTGGCTGGGGGGAA	41520
Qy	1561	gggggagggatagcatlaagagatalaccatagttaaagalyagltaaatgggtgcagca	1620
Db	41521	GGGGGAGGATAGCATTAGAGATATACCTATGTAAAGATGAGATTAATGGGTGACAGA	41580
Qy	1621	taccacaatvgggaacatgatacataacgtaacaaacctgcacattgtgcactgtaacct	1680
Db	41581	TACCAACAAGGAGACATGTATACATTAACGTAACAAACCTGCACATTGTGCATGTACCT	41640
Qy	1681	aggaacttaagtatataataaataaataataataataataaataaagattaaaaaac	1740
Db	41641	AGAACTTAAAGATATATATAAATAATATAAATAATATAAATAATATAAGATTAAAAAANC	41700
Qy	1741	tcatcaatgaacataattttttatctgtaaaaaatacttaaaaaaataaaacacttgat	1800
Db	41701	TCATCAATGAACATAATTTTTTATGTGATAAATAATCTATAAAAAAATAAACTTGAT	41760
Qy	1801	gtatccaactgtccacttttggcttggctgtgcctgtgcctgtgtgggtatactcaaga	1860
Db	41761	GTTATCCCATCTGCTCCATTTTGGCTTGGTCCCTGCTGTGGGGATTATCTCAAGAA	41820
Qy	1861	accttggccactccaatgtcctcttgagagatcccccacatglttctcttgtagagttcat	1920
Db	41821	ATCTTGGCCCATCCAAATGCTCTTGAGATGTCGCCCAAGTGTTCCTTGAGTAGTTTCA	41880
Qy	1921	ggttgatgtccaaagtcacatttbaacttgatttttgataaagaagaataagatgc	1980
Db	41881	GGTTGATGTCTCAAAAGTCCATTTTGACTTGAATTTTGTATATACCAAGATTAAGAGTC	41940
Qy	1981	tagttcatalcctgcatatgatalccagtttccagcaaatltiatgaaagalt	2040
Db	41941	TAGTTTCATTCATCTCATATGAGATATCCAGTTTCCAGCACAAATTTATGAAGGAT	42000
Qy	2041	gaccttccctatatctctgtgccttttgcataaaataagttcacctgtagatgtatgag	2100
Db	42001	GCTTGTTCCTTATATCTTGAGCTCTTGGCTTGGTGAATAAATAGTCACTGATAGTATGAG	42060
Qy	2101	ttctattctctgttctctatctcgtgtccacgtgcatagtgtcgttttcacagcaatc	2160
Db	42061	TTTATTCTGTGTTCTCTATCTGTCTGCCACGTGTCTATGTCTGTTTCATGCCAGTAC	42120
Qy	2161	tatgtcatttgggtgtgctatagcgtgtgtataaattgaaatcagaataatgatctctcc	2220
Db	42121	TATGCAATTTGGGTGCTATACCTGTGGTATATTTGAAGTCAGATAATATATATCTCC	42180
Qy	2221	taattatctcttggctccaatagccttggctcactcctcgggtcttttgggttccaagt	2280
Db	42181	TGAATTAATCTTTTGTGCTCAATAGCTTTGGCTACTCGGGCTTTTGTGGATCCATGT	42240
Qy	2281	aaatttgaatttttttcttctattctgtgaagaatgtcatgtgatlttggtaagta	2340
Db	42241	AAATTTTGAATTTTTTTTTTCTATTTCGTGAAGATGCTATGATTTTGTTAGTA	42300
Qy	2341	ttgcattgaacctgtagatgtcttgggtagatagaacatcttccaactataaagcatg	2400
Db	42301	TATGCAATTAATCTGTGATTTGCTTTGGGTAGTGAACAATCTTCCAAATCTATTAAGCATG	42360
Qy	2401	gaatacttcaatlttttttggggccctccaactcttltgcaaatlttagt	2460
Db	42361	GAAATATCTTCAATTTTTTTTTTGTGGCCCTTCAACTTCTTGTGTCAAAATTTTATAGT	42420
Qy	2461	ttcaaggtatagatcttccaactccttgtttaaatactagtaacttaattattattag	2520
Db	42421	TTCACGGTGAAGATCTTTCACCTCTTGGTTAATTACTAGTACTTATTTATTTATTTAG	42480
Qy	2521	ctatgttacaagatctcttcttgattctctttcagatgttccctgttagacata	2580

Dd	42481	CTATTGTTAAACAGATTACTTTCCTTGATTCTCTTTTTCAGATTGTCCCTGTTAGCATATA	42550
Qy	2581	gaatagtcggaattcttbyggccgggcggctggtcagccgcctgbaatccagaacttlygga	2640
Dd	42541	GAATAGTGTGATTTTGGGCCGGGCGGGTGCGTCAAGCCTGTAATCCAGACTTTGGGA	42600
Qy	2641	ggcgaagccgggcggatcaacgaagtcagagatcgaagcaatcccggttaacacggtga	2700
Dd	42601	GGCCAGAGCGGGCGGATACGAGGTCAGAGATYTCAGACACATCCGTGTAACACGGTGA	42660
Qy	2701	aacctgctctatbaaaacacaaaaatlaacggggcggtgtgtgacgggcgctgtgctc	2760
Dd	42661	ACCTGCTCTCTATTAATAACACAAAAATTAGCGGGCGCTGTGGCGGGCGCTGTGGTC	42720
Qy	2761	ccagctactcaagaaagcctgaagccagaaataagatgaaccgggaagccgagcgtcag	2820
Dd	42721	CCAGCTACTCAGAGAGCGCTGAGGCGAGAGAATAATGATGAACCGGGAGGCGCTGCAG	42780
Qy	2821	tgaagccgaagacgcgcaactgcagtcacagcctggcgaaaagaggagactccgtctcaa	2880
Dd	42781	TGAGCGGAGACAGCCCACTGCAGTCCAGCCGCGGCGAAAGGAGAGACTCCGTCCTAAA	42840
Qy	2881	aaaaaaaaaaaaaagaaagaaagaaagaaatgctglatcttltgatatgatlttgat	2940
Dd	42841	AAAAAAAAAAAAAGAAAAAGAAAAAGAAAGTGTGATTTTGTATGATGATTTTGTAT	42900
Qy	2941	actgtgacctctgtgaattgtgtatcaagttcaatgtgttcttlygtgagccttaagt	3000
Dd	42901	ACTGTGACCTGTGTAAATTTGTGTCAAGTTCTAATGGTTTTTGTGTGAGCTTTAGGT	42960
Qy	3001	ttcttcaaatbaataaagatcatcctgaaacaaaggaataatlygactcttcccttcaat	3060
Dd	42961	TTTTCCAATATAATAAGATCATCTGAAACAAAGATATTGTGACTTCTCTTCCAAT	43020
Qy	3061	ttgatgtccattctcttctctctctgtcgtatcaatagaagctccagtatatgtga	3120
Dd	43021	TTGTATGCCATTCTCTTCTCTCTGTCTGTATTCATAGGACTTCCAGATATATGTGA	43080
Qy	3121	aaaacagcgtgaagctgggacactctgtctctagaacttlaaggaagaagccttaagtt	3180
Dd	43081	AAAACAGTGTAAGATGGGCACTCTGTGTCTTAATCTTTAAGGAAGAGGCTTTAGTTT	43140
Qy	3181	ctccctatcatatgaatactagttgtctggtcatctcataatgagcttctctatgtag	3240
Dd	43141	CTCCCTATTCATATGANAAGTACTAGTGGTGCTATTCATATAGCCTTTCTATGTGAG	43200
Qy	3241	gtatgtccctctatatacaagttcttlyggaaatttatacatgaaggaatgttgaattc	3300
Dd	43201	GTATGTCTCTCTTATACACAGTTTTTGTGGAAATTTTATCAAGAGGAGTGTGAATTTT	43260
Qy	3301	atcaactcgtcttcttagagatacaactcgaagaatgaatagatgtgttctgtccctcatctga	3360
Dd	43261	ATCAACTGCTTTTTCAGCATCACTAGAAATGATAATATAGGTTTTGTCTTATTTCTGTA	43320
Qy	3361	gataagacatatcacagttgttgaattgtcatatgtcacaaccaaccctlycatccctggagat	3420
Dd	43321	GATAAGACATATCACAGATGTTGATTGTGCATATGTCCAACACCCCTGCATCCCTGGAT	43380
Qy	3421	aaatcccaactgatacgaatgaatgaatcttlttaataigtgttgaaccagttgtcag	3480
Dd	43381	AAATCCCACTTGATATGATGATGATATCTTTTAAATATGTTGTGAACCAATTTGTGATG	43440
Qy	3481	tatttgcctcgaagattcttaacaaatcttaacgaagatactggccgttagctctctt	3540
Dd	43441	TATTTTCTCGAGGATTTTTCATCAATTTCTACAGAGATACCTGGCCGTGTACTTTCCTT	43500
Qy	3541	tttltgatctattgtctgtgttlttgatcaaggtlaaactgagcctgttgaatgagttc	3600
Dd	43501	TTTTGATGTACTTTTGTCTGGTTTTGTGTATGATGAGGTATATAGGCCCTGTGAATAGATT	43560
Qy	3601	tggaaatattccctccctctctatgatttccagaatgtttgagatcagttgtatagtac	3660
Dd	43561	TGGAGATTTTCCCTCTCTCTATGATTTTCAGAGTATGTTGATGATGAGTGTGATATAGTTC	43620

OY 3661 tcaagctcttgtagaattcaagcagtgaaatacttcgggtcccaagatcttgcttactgtt 3720  
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Db 43621 TTCAAGCTCTTGGTAGAATTGACAGAGTAATCTCGGGTCCCAAGATCTTGTAATTGTT 43680  
OY 3721 attatctctgtagaagtttagaattcttcgaaggtcccaatatttgtagagtgatgtat 3780  
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Db 43681 ATTATCTGTTGACAGTTTGTACATTTCTTCAGGGTCCAAATATGGATGATGATGAT 43740  
OY 3781 aggaattatatacatctcttcagatttcccaattatctgcataatactgctcagtag 3840  
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Db 43741 AGAGATTATATCATTTCTTCTAGATTTCATATTATTTGGCATATATTTGGCATAGTAG 43800  
OY 3841 ccaacatgatcccttggaattctglatatcaagtgtaagtctcccttcattcttg 3900  
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OY 3901 attatattatcttggtct 3960  
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OY 4141 tgaagagtgtagaattatcttgagctcttgacattagagactgttgtaacctgctcc 4200  
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Db 44221 ATACAGAGCAACCCAGTGCAGTATGCTATGCTTTGAGACTTATAGAGTACAC 44280  
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Db 44341 TCTCTCCCTTACTTTCTCCCAAACTGAGTCTATTTCTGTGAGTGTCTT 44400  
OY 4441 ggaagctgggggtggtgacacaaagcactgtggtctaccatcctgaagctgagctgg 4500  
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Db 44401 GGAGCTGGGGGTGGGTCACCAAGCAACCTGTGTGCTACCATCTAGACTGACTGG 44460  
OY 4501 gtcagacctgaagctagcacagcactgatactgcacaaagccccactgtgactactaca 4560  
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Db 44461 GTACAGACTGAAAGCTAGCACAGCACTGGATATGCCCCAAGGCCACTGTGACTACTACA 44520  
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Db 44521 GGGTACACACATTTTGTCTCAAGGCTCTAGCACTTACCAATCAGCAGTCAAAAGCCAG 44580  
OY 4621 ccaagttgtgtctctccctcaggtgtagaagttctccagccccagggaggtgccaca 4680  
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Db 44581 CCAGGTTGTGTCTTTCCCTTCAGGGTATGATAGTTCTCCAGGCCCCAGGAGGTCCACA 44640  
OY 4681 gatgcacatcggaggttggtctctctctctctctctctctctctctctctctctctct 4740  
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Db 44641 GATGCCATCTGGAGTTGGGTCTCTTATTTTATAGTTAGGAATAAAGATAGCATGCTA 44700

OY 4741 tgaattccaactcccatcttccattaggtatctctctggaatglttccaactcgtctcta 4800  
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Db 44701 TGTATTTTAAACTTCATCTTTCATTTAGGTATCTCTGAAAGTTTTCATCTGTCTCTA 44760  
OY 4801 ctctacgtccaacaaaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 4860  
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Db 44821 GATGATGGAAGAAGTAACACAGCTTTCCCAAGGTACATTAAGACACAAATTAACAGTAAT 44880  
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Db 44941 TGAGACAGAGTCTGCTCTGTACCCAGCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGT 45000  
OY 5041 gcaacctcgcctccctgggttcaagcgatctcctgtctcaagctcctgagtagctgga 5100  
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Db 45061 TTACAGGTGTGTCACACGCGCGCTGTGCTAATTTTGTATTTTATTTAGTAGACAAAGTTTC 45120  
OY 5161 accatgtgtgtcaggtgtgtgtcttgaaactcctgaaactggtgtgtgtgtgtgtgtgtgt 5220  
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Db 45121 ACCATGTTGTGACAGCTGTGTGTGAAGTCTGACCTGTGTGTGTGTGTGTGTGTGTGTGT 45180  
OY 5221 caaagt 5280  
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Db 45181 CAAAGT 45240  
OY 5281 ccaactctcgcct 5340  
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Db 45241 CACACT 45300  
OY 5341 acacaacagacagaggggaaataaaggaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgt 5400  
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Db 45301 ACACAACAGCAGCAGGAAATAAAGGAGAGTGTGGGTGGGCGAGTGCATCATCT 45360  
OY 5401 gtaatccagcactttgggaggtctgaggtcggaagatcaagaggtcagggatctgagacc 5460  
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Db 45481 GGTGGGGGGCGCTGT 45540  
OY 5581 ccgggaggtcggaagcttgagtgagccaagatctgcgcaactgcacagcctgggagca 5640  
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OY 5641 gaatgagactctgtctcaaaaaaataaagaaagaaaggaaggtgtgtgtgtgtgtgtgt 5700  
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Db 45601 GAATGAGACTGTGTCTCAAAAAAATAAAGAAAGAAAGAGAGTGTCCCAAAATTA 45660  
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OY 5761 aaatcactgcacttctcccggaatagcacagaagtgtcagatcttctcaagcgaatgt 5820  
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Db 45721 AAATCAGCACTTTCTCCCGAATAGCACAGAGGTGAGATTTCTTCAACGCAATGT 45780  
OY 5821 gaaacacatttctcagattaaagaagaatgtgtataggggaataatgcagcgaatgtctcc 5880

D	b	45781	GAAACATTTTCTAGATTAAAGAAAGATTGGTATAGGAATTAATGCAGCATGCTTCC	45840
Q	y	5881	taattgcttagaaggTccgtgttcaatgaattatctcttttataaagaattaat	5940
D	b	45841	TAAATGCCTAGAAGGCGCTGGTTCACTAATATTATCTTTTATAAAGATTAA	45900
Q	y	5941	aattcttaataccaatgtgcttaattttctcttctctttttttttttaagaaag	6000
D	b	45901	AATTTCTAATTAAACAAATGGTAATTTTTCCTTTCTTTTATTTTAAAGACAG	45960
Q	y	6001	gtctctgtctgtccccaaggtctgaagtgcagtggagcaatccggtcacgcgaagcc	6060
D	b	45961	GGTCTTGCTCTGTCCCAAGGCTGGAGTGCATGGAGCAATCCGGCTACTGCAGCTC	46020
Q	y	6061	cgctccctgtcacaagtgaatcctctcaaccacagctccctctagctggtggctacagca	6120
D	b	46021	CGTCTCTTTGGCTCAAGTGTACTCTCTCACCTCAGCCCTCACTAGCTGGGGCTACAGCA	46080
Q	y	6121	cgtagcacacacccccaaactttttgtatttttggagatgaggtttgtgcagtgtg	6180
D	b	46081	CGTGCCACACACCCAACTAATTTTGTATTTTGGAGAGAGGTTTGGCATGTTGT	46140
Q	y	6181	ccaagctgtgtcttgactctctgtggtcacaagtatccacactgtctggtctcccaagtgc	6240
D	b	46141	CCAGCTGGTCTTGAACCTCTGGGGCTCAAGTATCACCTGATCGTGCGGCTTCCAAAGTGC	46200
Q	y	6241	tgggaattacaggcaatgagctgtgcttgaatttttcaataaaatcatcacaataaata	6300
D	b	46201	TGGGATTACAGGCATGAGGCTGGCCCTGTGATTTTTCAMAAATATCTTCACAAATMAATA	46260
Q	y	6301	aaaactctgtgcagactatgtatctcagtttctgttgccttggaagaagagctacgctatc	6360
D	b	46261	AAAACTCTGTGCACACATATGATTTCTGAGTTTGGCTTGGAAAGAGGACTACGGTATC	46320
Q	y	6361	tttaagagctctctctcttctgtggttcagaagtctgttcttgttgaagctgttaaagctgtg	6420
D	b	46321	TTTAAAGACTCTCTCTTGGGTTCAGGCGCTGGGTTGGTAAAGTTGTAAAGGTTGT	46380
Q	y	6421	ctttgtcttatttttcaaccctcttaagctgtatctctcttcaacaggtaaacattttctcta	6480
D	b	46381	CTTTGGTCTTATTTTCAACCCCTTTAGCGTACCTCTTCCACAGGTAACATTTTTCCTA	46440
Q	y	6481	ctgtgaattttccagtgactcacaagagatgcacattatatttcattgtccaaagacttgt	6540
D	b	46441	CCTGGAAATTTTCCAGTGACTACAGAGTCCATCTTATATTTCCATTGGCTAAAGACCTTGT	46500
Q	y	6541	tttcaacagtggttcacattaaagaacataatgtattatatactctctgagaatgtctgcggg	6600
D	b	46501	TTTCAACGTGTGCATTTAAACACATATATTTATATCTCTTGAGAAATGGCTGGGG	46560
Q	y	6601	agaatgggggtgaactttttaagcttcaaaagccatgaagatgacaagtcaatgtcaggaccta	6660
D	b	46561	AGAAATGGGGTGACTTTTAACTTCAAAAGCCATGAAGATCAAGCAATGCAGGCACTA	46620
Q	y	6661	gggggaatggttttcaatgggctgtgaaggtgtgcagggtgtcatctgtatcccttccaatt	6720
D	b	46621	GGGGTAAATGTTTTCAAATGGGCTTAAGGTGGCAGGGTGCATTGTATCCCTCCAAAT	46680
Q	y	6721	caactatgaagagcgtcaccacacgtgaagaagcctttgtttaaagaattctctcagaagc	6780
D	b	46681	CACCTTATGAAAGGCACTACCCACTGTGACAGGCCCTTTGTTACAAAGATTTCCTCCAGGAC	46740
Q	y	6781	acaacagcaatttgaatgggaactaaatlattaaagcaggcacatatatagaagggtgataagc	6840
D	b	46741	ACAACAGCATTTTGAATGGGACCTAAGTATTTAAAGCAGGCATATATTAGAGGGTGGATAGC	46800
Q	y	6841	ctgtgtcaaaaattctagaagtcagatagacagggttccaatctcctagctatacttttac	6900
D	b	46801	CTGTCCAAAATTTATAGAAGTCAAGTATAGCACCGGGTCCAAAATCTTAGCTATATCTTTTAC	46860
Q	y	6901	tttgaacctcaaggaaaggctgtatgtctcttgggtctcagtttttctcatgtcatataaa	6960

D	46861	TTGACAAC	TACGAGAAAGG	CTACTAGTTC	CTCTGGGTCT	CAATTTTCTCAT	TATCAATATAA	46920
Q	6961	atgagagataa	aataa	ctcaaggagctg	taagaataa	catcagtaac	tagcagatga	7020
D	46921	ATGAGAGAT	AAAAATAT	CTCTCCAAAGCA	CTGTAAAGAT	AAATCATGAC	TACCAAGTGA	46980
Q	7021	ctggcatatg	gtgaaatg	taagaagtag	tataatcc	atgaaataa	attgaaag	7080
D	46981	CTGGCATATG	GTGAATGAT	AAAGATAG	TATAAATTCACAT	GAAATATAA	AAATTTGAGG	47040
Q	7081	aaccagaat	taagagataa	aaagaagaaata	ctgagaggtg	agagtag	ctcagaat	7140
D	47041	AACCAAGAT	TAGAGAT	ATAAAGAA	AAATTTGGAGG	TGAGGTGAGG	TAGCTCAGAGTAT	471000
Q	7141	ctaattacc	ctgcatctgt	taaalatcc	aaactaaga	agctaatg	caatgaa	7200
D	47101	CTAATTAAC	TCTGATTTG	TAACTCAAA	CTTAAGAGCT	TAATGCAAA	TGACTTGAGAA	471600
Q	7201	tagtbtacca	agttcatcc	acttgaagctt	cttcgcata	tfgtggatata	tagaaggtgc	7260
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D	47221	CCGCATGT	CTTATATNG	CTTGCAACAGCTCC	CAATTTGCCAT	TATATAGCAAC	GACGAG	472800
Q	7321	tccatattat	gtccctgtgt	gtcatatata	atataatga	atgactctt	gtgaaatgt	7380
D	47281	TCCATATTTAT	TCCCTGTGTCT	ATATATATAT	TATATATATGAT	ATCTCTTGAA	GAATATG	473400
Q	7381	agatttgaa	caaatg	aatttcc	acagtcac	ctacata	tagaagatgt	7440
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D	47701	TGGAACTTTT	ACATTTTACT	ATAGTGTGCTGT	TTTTTTTTTTT	CTTAAATCTT	AAAAATTC	477600
Q	7801	agcttcca	agatcc	cttgacatcc	cccaagcc	agataat	cttaattg	7860
D	47761	AGCTTCCA	GATCCCTG	TGACATCC	CCAAAGCC	AGTAAATCA	ATTTTGAAAT	478200
Q	7861	caaaatgt	cttccat	acatact	tttgt	taagagata	ctccag	7920
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D	47881	CGTGCAT	CAAGCCCTC	AGAGAGTCT	TAAAGGAC	AGAAAGAGG	GTGACAGGCTCAGAGAGG	479400
Q	7981	aagttg	ctctgc	agagctag	tgaagagagc	ctccagctcc	ctctctct	8040
D	47941	AAGTTTGG	CTCTGC	AGTCTCT	AGTGAAGAGG	CTCCAGCTCC	CAATTTCTTGTGGGCAATG	480000

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D	51301	AAAAAAAAA	TTAGCC	AGGTGT	AGTGGC	ACATGT	CTGTGT	GGTCC	CACTT	CTCAT	GAGG	GGCTG		51360		
OY	11401	tgtgtg	ggagaa	tgcgtt	gagact	tggag	tggat	gaagt	tga	agtgaa	ctg	atga	catga	cgac	11460	
D	51361	TGGTGG	AGAA	TCCG	TTG	AGACT	GGG	AGTT	AGGTT	GAAGT	GAAGT	GAAGT	GAAGT	GAAGT	51420	
OY	11461	ctcact	ccccca	ctgg	tgc	agag	taag	at	ccat	ctc	caaaaaa	atat	atat	at	11520	
D	51421	CTCACT	CCCCCA	CTGG	GTGAC	AGAGTA	AGATTC	CTCA	CTCA	AAAAAA	AAAAAT	ATAT	ATAT	ATGT	51480	
OY	11521	atatata	tatag	agag	agag	agag	at	gtat	gtt	gtg	aaatg	ctg	aaag	atga	gaag	11580
D	51481	ATATAT	ATAT	ATAG	AGAG	AGAG	AGAT	ATGT	TTGTT	GTGA	ATGT	GCAG	AGAT	GAG	AG	51540
OY	11581	catcag	gaag	tgt	ctaac	agag	at	tgt	tgc	aaac	at	cg	ct	tg	ctc	11640
D	51541	CATCAG	CGCAG	TCTTA	CCAG	AGAT	TGTGT	GAC	CAAC	AT	CGCG	TGG	CA	CTCT	TGTGC	51600
OY	11641	acggtc	actgc	caaga	caac	cgga	acc	atga	at	gc	tgt	ttc	ga	act	gc	11700
D	51601	ACGGTCA	CTGCA	GCAGCA	CAACG	GAAC	CTGA	AGTGT	CTGT	TCG	AGACT	TCG	AGAG	CACT	TAAT	51660
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REFERENCE	AC009264	Submitted (10-AUG-1999)					
AUTHORS	Bubb,K.L., Desmarats,C.L., Ramsey,S.A. and Hubley,R.M.						
JOURNAL	Direct Submission						
TITLE	Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA						
REFERENCE	On Nov 17, 1999 this sequence version replaced gi:5788037.						
AUTHORS	Sequence Quality Assessment:						
JOURNAL	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.						
TITLE	All manually edited bases have been reduced to quality zero.						
REFERENCE	Quality levels above 40 are expected to have less than 1 error in 10,000 bp.						
AUTHORS	Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.						
JOURNAL	*****						
TITLE	NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.						
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AUTHORS	735	gap of unknown length					
JOURNAL	1611	contig of 877 bp in length					
TITLE	1612	gap of unknown length					
REFERENCE	2286	contig of 675 bp in length					
AUTHORS	2287	gap of unknown length					
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TITLE	2965	gap of unknown length					
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JOURNAL	4554	contig of 807 bp in length					
TITLE	4555	gap of unknown length					
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AUTHORS	5434	gap of unknown length					
JOURNAL	6862	contig of 1429 bp in length					
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AUTHORS	10363	gap of unknown length					
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AUTHORS	11299	gap of unknown length					
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OY	1794	-----	1794
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OY	1794	-----	1794
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OY	1794	-----	1805
Db	51427	gtaattcttcaacttgttgattgttttcttcttgctgtgtccgaagcttttttaactttcatgtaac	51366
OY	1806	cccatctgcacatttttgctttgtgtgtcgtgtgtgttggggtatatactcaagaacatt	1865
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OY	1866	tggcaccatcaatgtcccttgagagatgtccccaatgttttctgttagtattgtcaatgtt	1925
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OY	1926	gattgtcca-----aaagtcatttgaacttgatttttgtatataagcaagagat	1973

Db	51248	GTACTCTTAAGATTTCAGCTCTTTTATTTTCATTGTTGACTTGGCTTTCTATATATGTGTAAGAAT	5118
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Oy	2150	catgcacgactcatgctacttgggtgtgcatacg--ctgtgtataacttgaatgcagata	2207
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Oy	2208	atagactccctccgtgattatctcttcttgctccagatagctgtgcactcgtgtcctt	2267
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Oy	2432	tcaactctctgtgtcacaacttataagtttccaagtgtagagatcttccactcttggct	2491
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Oy	2492	aa-----tiactaggtacttatttattttagctatgtagtaaaagattactcttg	2546
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Oy	2606	cgtgtgtcagcgccttgaatccacagactttggggggccggggcggtgtcccggt	2665
Db	50539	ACTTTGTATCTGCACACTTATTAAGTATTTATTCATTTCAAAAGTTTTTTAGTACGTC	50488
Oy	2666	caggagatcagagaccatccctgtgtlaacaacggtgaaacctgtctctatlaaacaacaaa	2725
Db	50479	TATGTTTTTTCAAATPAAAGATCATATTTATCTGCAACATGAAATPAAATTTGACTTCTTCCA	50428
Oy	2726	aaatttagcggggcggtgtgtggcgggcgccgtgtgttcccgactaccacggaggcgtgaaggcag	2785
Db	50419	TTTCAGTTTGGATGCAATTTTCATTTCTTTCTCTGTGTGATGTCCTAGATTAAGACTTCTAG	50366
Oy	2786	gagaatagagtgagaccgggaagcggaagcggtgcagtgcgcgagacagcgca-----	2838
Db	50359	TAAACATCTCAATTAAGAGTGAAGTGCACATATCTATTTGTGCTCCAGATCTCAGTGCAGAG	50300
Oy	2838	-actgcagtcacagctctgggcggaagagggagactccgtctcaaaaaaaataaagaaa	2896
Db	50299	GCTTTACGTTTTTTTTTTTATTCAGATATATTTTATGCTATGGGTCTGTGCATATATGTGCTT	50241
Oy	2897	aagaaagaaaagaaatgcgtcgtatttttagtagaattgttctatcgtgtgacctgtga	2956
Db	50239	TTATGTGTTGAGGTATATTTCTTCCACAAACAGTTTTTAAGAGTTTTTATCATGAAGGG	50188
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 Db 49399 ATTTATTTGCTTTGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 49340  
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RESULT 5  
 AC009794

LOCUS AC009794 152794 bp DNA HTG 03-DEC-1999  
 DEFINITION Homo sapiens chromosome 4 clone RP11-343C10 map 4, \*\*\* SEQUENCING  
 IN PROGRESS \*\*\*, 33 unordered pieces.  
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 HG: HTGS\_PHASE1.  
 KEYWORDS human  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 152794)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
 Baker,J., Baldwin,J., Barna,N., Beckert,R., Benn,J., Brown,A.,  
 Castle,A., Cerny,J., Collangelo,M., Collins,S., Collymore,A.,  
 Cooke,P., DeRubeis,K., Depayre,E., Devon,K., Dewar,K.,  
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 Funke,R., Gage,D., Galagan,J., Gerdyne,S., Gilbert,D., Grant,G.,  
 Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,  
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 Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,  
 Meidrum,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,  
 Naylor,J., Nijhoff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,  
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 Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,  
 Teichgraber,S., Toruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,  
 Wheeler,J., Wu,X., Wymann,D., Ye,W.J. and Zody,M.  
 Direct Submission  
 Submitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Dec 3, 1999 this sequence version replaced gi:581556.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 COMMENT  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submission@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L2049  
 Center clone name: 343\_C\_10  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 33 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1 1032: contig of 1032 bp in length  
 \* 1033 gap of unknown length  
 \* 2235 gap of unknown length  
 \* 3449: contig of 1215 bp in length  
 \* 3450 gap of unknown length  
 \* 5336: contig of 1887 bp in length  
 \* 5337 gap of unknown length  
 \* 7197: contig of 1861 bp in length  
 \* 7198 gap of unknown length  
 \* 8859: contig of 1662 bp in length  
 \* 8860 gap of unknown length  
 \* 10391: contig of 1532 bp in length  
 \* 10392 gap of unknown length  
 \* 12405: contig of 2014 bp in length  
 \* 12406 gap of unknown length  
 \* 14442: contig of 2037 bp in length  
 \* 14443 gap of unknown length  
 \* 16847: contig of 2405 bp in length

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Matches 2741;	Conservative	0;	Mismatches 1020;	Indels 201;
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OY	232	gcatgtgtaagataatccttaagcaaaagaacaaagcttggaggaatcctgtcactgtact	291
Db	29938	ACATTGGCCAGACAACTCCTAAGCCCAAAAGAACAAATCTGGAAAGCATGTCTACTGTGAC	29937
OY	292	tcaacttactacaaggctcactagta-----acccaacacga	329
Db	29998	TCAAACTTACACACAGGGGTACAGTAAACAAATGTGTGTGACTGTGTACCAAAACAGTA	30057
OY	330	tgttacttgcaccaaacaagaataatagaccaatggaaatggacacagatccctcagaata	389
Db	30058	TGTGACTGTGACCAAAACAGAGATTTATGACCAATGGAACAGAACAGAGCCCTCAGAAATA	30117
OY	390	ataccacacatcttaaacacatctgtctctttgacaacctggaaaaagaagaataatagga	449
Db	30118	ATGCCACATCTTACAACTATCTGTGATCTTTGGCAAACTGACAAAAACAGAAATGGGA	30177
OY	450	aagatctccatttaacaaatgtgtgtcgtgggaaaaactggctagccatatgttaagaagctg	509
Db	30178	AAGATTTCATATTTAATAAATAGTGTGGGAAATGGCTATGGCATATGTGTGAANAAGCTG	30237
OY	510	aaactgtgacctccctccctccacactatcaaaaaatlaataagaatggatataaagactta	569
Db	30238	AAACGGATCTCTTCTCTTACACCTTGT--AAATTAATTCAGATGTGATTTAAACATTA	30294
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OY	629	ataggcatgggcaaggacttcattgacttgaacaacccaagaacatgtgcacaaacacaa	688
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Db	30827	TACACTAATTCAACCATTTGTGGAACACGTGTGGATTTCCCAAGGGGTGTGAACATA	30886
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OY	1226	ctgcataaagaacacatgacatgtatgtttatgttggcacatcacaacatagcaaaagac	1285
Db	30947	CTACATATTTTTCTTTCTTCCACACGNTTATATGCTTCTGTGGGTGGTACAAAGACT	31006



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OY	1346	caacgtggaatactctgaccccaataaagaagtgaagttcaagtcctctgtgaagaatg	1405
Db	31067	CACCATGGAAATCTATGCGCCATATAAAATGATGACTTAATGTCTTTTAGGACATAG	31120
OY	1406	atgaagctggaaacatcctctcgacaactatccacaagaagtaganaaaccaaacccac	1465
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OY	3552	ttttgttcggttttgatatcaagggaactactgaccttgyagatgaqtlttgaaagtacc	3611	
D	33178	GTTTACTAAATTTTAGTAATCATGATTAATTTCTTCATTTGTAGAATAGATTAGAGAGATC	33237	
OY	3612	cctctctctctaagtttccaagtagtttgagtaagytgtatc---agttcttcaagtc	3668	
D	33238	TGTCTCTCTAGATTTTTTAAAAATAAGTGTACAGAGAGATTGGTACTGTGCTGTCTTTGTATG	33297	
OY	3669	ttttgtagaattcacagcagtgaaatactctgggtgccagatctgtc-----	3714	
D	33298	TCTGATGAATTTTGGCTGTGAATFACGTCTGTTTGCAGAGATCTTTTGGTTAGATGTTTC	33357	
OY	3714	-----actgttatattatctgttccaagttttagatttcttcagg	3752	
D	33358	TATTAAGTATTCATTTTCAGAACCTCATTTCTAATGTGTCAAGGTTTGAAATTTCTCTTGC	33417	
OY	3753	gtccaatittggttagatgatgtatgtataggagtttatacatcttcttcagaatttccaa	3812	
D	33418	AATCAATCTCAGAGAGGTTGTATGTTTCCAAGGAATTTATTCATTTCTCAGATTTTATNC	33477	
OY	3813	tttatgtgcataaattgtctcatagtagccacaataatgactcttgaatttcgatatc	3872	
D	33478	TTTTTGTATTAGAGAGATTTATTAATAGCCTTAAGAGATCTTTGTATTCTGTGGATC	33537	
OY	3873	agttgtaaityctctctcttccattctcgatttattattatggatcttctctctcgtt	3932	
D	33538	AGTTAATATGTTTCTTGTCTCATTTCTGTACTGTACTTATTATTACCTTCTCTTTTTP	33597	
OY	3933	ct 3934		
D	33598	TT 33599		
RESULT	6			
AC007282/c				
LOCUS	Homo sapiens clone NH0484N09, *** SEQUENCING IN PROGRESS ***, 4			
DEFINITION	AC007282 192151 bp DNA HTG 05-JUN-1989			
ACCESSION	AC007282			
VERSION	AC007282.2 GI:5001487			
KEYWORDS	HTG; HTGS_PHASE1.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	1 (bases 1 to 192151)			
JOURNAL	Waterston,R.H.			
REFERENCE	The sequence of Homo sapiens clone			
AUTHORS	Unpublished			
TITLE	2 (bases 1 to 192151)			
JOURNAL	Waterston,R.H.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (09-APR-1999) Genome Sequencing Center, Washington			
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis			
JOURNAL	MO 63108, USA			
COMMENT				
	On Jun 5, 1999 this sequence version replaced gi:4580496.			
	* NOTE: This is a 'working draft' sequence. It currently			
	* consists of 4 contigs. The true order of the pieces			
	* is not known and their order in this sequence record is			
	* arbitrary. Gaps between the contigs are represented as			
	* runs of N, but the exact sizes of the gaps are unknown.			
	* This record will be updated with the finished sequence			
	* as soon as it is available and the accession number will			
	* be preserved.			
	1 5124: contig of 5124 bp in length			
	* 5125 5141: gap of unknown length			
	* 5142 32144: contig of 27003 bp in length			

	* *	32145 32162	32161: gap of unknown length contig of 73599 bp in length	
	*	105761 105778	gap of unknown length contig of 86374 bp in length.	
FEATURES				
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			/organism="Homo sapiens" /db_xref="taxon:9606" /clone="NH0484N09"	
BASE COUNT		62623 a 38154 c 35320 g 56003 t	51 others	
ORIGIN				
Query Match	Best Local Similarity	6.4%; Score 1592.6; DB 33; Length 192151; Matches 2839; Conservative 68.6%; Pred. No. 4.5e-266;		
OY	1	aggacctcttaagygagaactacaacaccatgcttcacgcgaagttaaagagacacaaca 60		
Db	60238	AGGACCTCTTAAGAGGAGTACTACAACACTCTGAGCAAGAAATATAAAGGTATCAAACA 60179		
OY	61	aatggaaacaacattcccatgctcctgatgtaggaaaataaatcaatatctgtgaanaatggccatc 120		
Db	60178	AATGGAAAGAATTTCATGCTCATGCGTGTTAGGAGAGATCAATATCCTGTGAANAAGGCCATAC 60119		
OY	121	tgtctaagtgtaattatagatgccatgscatcccacccaagcttacaatgactttcttca 180		
Db	60118	TGCCCAAGTAAATTACAGATTCAATGCATGCCATCCCATAGGTACCATATGACTTCTTCA 60059		
OY	181	cagaattggaaaaatctactttaaagtccatatggaacccaataaagagcctgcattgtca 240		
Db	60058	CAGAAATTGGAAAAAGCTCTTTAAAGTTCATATGGAACCAAAAAGAACCCGCAATTGCCA 59999		
OY	241	agataatcctaagcaaaaagaacaagctltggagcgatcatgcttactgacttcaaactat 300		
Db	59998	AGTCATCTCTTAAGCCAAAGAACAAAGCTGGAAGGATCACACTACTTCACTTTCGAACTAT 59939		
OY	301	actacaagctactagtaaaccaaaaacagcatgctggtlaccocaaaaacagaataatagasc 360		
Db	59938	ACTACAAAGCTACAGTAAACCAAAACAGCATGCTGTAAGTACCACCAAAAGAGATATAGATC 59879		
OY	361	aatggaatvggaacagatccctcagaataataccaacacatctaacacatctgactcttg 420		
Db	59878	AATGGAAACAGACGAGAGCCCTTAGAAATTAAGCCCATATCTACACACTATCTGATCTTTG 59819		
OY	421	acaaacctgaaaaagacacaagaataatagggaaaggaattcccttaattaataatggtgtcgg 480		
Db	59818	ACAAACCTGAAAAAACAAGCAATGGGAAAGGATTCCTTTAATTAATTAATGATGCTGGG 59759		
OY	481	aaactgctgctgcacatagttagaaagctgaaactggaactggatccctctccacctatacaa 540		
Db	59758	AAAACCTGGCTGCCCCATTAAGTGAAGAGCTGAACATGGATCCCTTACACCTTAATACAA 59699		
OY	541	aaattaatctcaagatggatlaaagact--aaatgttagacctaaacataaaaaaccta 599		
Db	59698	AAATCAATTCAGATGGATTAAGCTTTAAAGCTTTAAACGTTBACTTAATAATATAAAAAACCTG 59639		
OY	600	gaag--aaactagggcaatatcacattcaatagacatlaggcattggccaaggaacttcatgactgaa 658		
Db	59638	GAAAGAAACCTTAGGCATTATACCATTCAGGACATAGGCATAGGGCAAGGACTTCATGCTTAA 59579		
OY	659	aacaccaaaagaatatgggcaaaaaacccaataatlgcaaaacaggaatcgaatlaaataaag 718		
Db	59578	AACACAAAAGCAATGGCAACAAAGCCTTAATTTGCAAAATGGGATCTAATTTAACTTAAG 59519		
OY	719	agcttc-tgaaacagcaaaaagaa--atatcataagatgtaacagggcatccctacaagaatggga 774		
Db	59518	AGCTTCTTGACAGCAAAAGAAACTACCATCAGATGAACAGGCAACTACAAATATGGGA 59459		
OY	775	gaaaatttttacatctaccatctcgtgaacaaagggttaataiccgaatcttcaaaagaact 834		
Db	59458	GAAATTTTTCCCACTATCTATCTGCAAAAGGGCTTAATATCCAAATCTCAATGAAGCT 59399		

Oy	835	taaaacatttgcagaagaaaaaatcaaacaccctcataaaaagtggcgaagaatgca	894
Db	59398	CAAAACAATTTCACAAAAGAAAA-----AACAACACCCTATPAAAAAGGGGCAAGACATCGA	95344
Oy	895	acagaccttcataaagaagacatttatcgccgccacagacaatgtaaaaatggtcat	954
Db	59343	ACGACACTTCTTAANAGANGACATTATTGCAGCCAAAAAACCTGTGAAAAATGCTCTC	95288
Oy	955	catoactgpcatcacagacatgycaaatccaataaaaccaatatgatalacatctcacccag	1014
Db	59283	CATCAGTGCCCATCAGAAGAAATGCAATCAAAAACCAATGAGATACCATCTCACACAG	95222
Oy	1015	ttagaatgycatcatctaataaagtcaggaaacacacaggtgctgtgagagatgtygagaaa	1074
Db	59223	TTAGAAATGGCAATCATTTAAAAAGTCAGGAAMCAMCAAGTGGTGAGAGATGTGGAATAA	95166
Oy	1075	taagaaacacttttaacactgttggtggagactgtraaactagcttcaacacttgtgsgaagacag	1134
Db	59163	TAGAACACTTTTACACTGCTGTGGAGCTGTGAACCTAGTTCAMCCATTGTGGAGACAG	95100
Oy	1135	tgtgpgcattctccaagagatctagaactlagaataitcatlttgaccagcccatccattac	1194
Db	59103	TGTGGCCATTCTCTCAGAGATCFGAACCTGANAATACATTTGACCAGCATTGCCATTAC	95044
Oy	1195	tgggtatgtatccccaaaggattataatcatcgtcgtctataaagaacacatgycatgtatgt	1254
Db	59043	TGGGTATATCCCAAAGGACTATTAATCTAGTGTGTATAAAGACACATGCAACATATTTGT	95898
Oy	1255	ttattgtgacatcttacaatatagacaagaagcctgtgaccacaaccacaaatgvtcatcagtg	1314
Db	58983	TTATTTGGGCAATTATTCACATATGCAAAAGACTTGGAAACCAACCAATGTGGAACATGA	58922
Oy	1315	tagactggaatltaagaaatgtgycatgyltalacacaglygnaatlathtgacccat-aaaa	1373
Db	58923	TAGACTGTGATTAGAAAAAGTGGCACTATACACCATGGAATACTATGACACCATATAAAA	58866
Oy	1374	agagtagttcaagtcctcttttagagagacatgaatgaatgttgaaacccatcattctlgca	1433
Db	58863	ATGTATGTTTCATGTCCTTTGTATGGGACATGTGATPAAAAITGGAATCTCATTTCTCGTA	58800
Oy	1434	aactatcacagaagatagaaaaccaaacaacacatgttctcatcatagtlgysaatlgaa	1493
Db	58803	AACATGCGACAGAACAAAAAACCAACGCCACATTTCTGCATCATAGTGGGAATTGAA	58744
Oy	1494	caatgagacaacttagacacagggtyggggaacatacacaccagggcctgtcgttggcgtg	1553
Db	58743	CAATGAGAACACATGAGACACAGGAAGGGGCAACATCACACTCTGGGGACTGTTGGGGGTG	58684
Oy	1554	ggggggaaggggggggatgcatgcatllggagatrlactactatgtlaaagaatgagttaaagg	1613
Db	58683	GGGGGAGAGAGGGGAGATAGCATTTGGGAATATPACTTATGCTAGAGAGTAGATTATGG	58622
Oy	1614	tgcagcatcacacaatggygacatgtalacataagtlaaacaactgycacatltgycat	1673
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Oy	1674	gtacccttagaactlaaaglatatataaataataataaataaataaataaataa-----	1729
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Oy	1729	-----	1729
Db	58505	AGTATCCGTTTATGTCCTTGTCTGCTTTTTTAAATGGGGTGTGTTGTTTTTCTGTAAA	58440
Oy	1729	--gatataaaaaactcatcaatgaanaactattttcatcgatataaataatctcaaaaa	1786
Db	58445	TTTGTTTAAATGTCATATAGATGCTGGATATTAGACCTTTGTTTGAATGCAATGTTTGCA	58388
Oy	1787	aaaaaaaaac-----	1796
Db	58385	AAATATTTCCCCCATCTTTAGGTTGTGCTGTACTGCTGTGATTATTTTGCTGTGCAGAA	58322
Oy	1796	-----tgaatgtlatcccatctgcatcttgccttgcgttgcgtgctgtg	1845

[illegible]

Dp	57299	CAGGATTTCCATGCGATGTGTACTAGAGAGTGGTGAGAGAGGCGACATCCTTGCTTGTCG	57239
Qy	2883	aaaaaanaaagaanaaagaanaaagaatgcgatttttgcatagaatcttgatc	2942
Dp	57238	AGTTTTTAAAGG----GGAATFAGGAAATTCGTTTGATTTACATCCATTTTGTGAAGCA	57183
Qy	2943	tgtgacctgttgaaatttgcatacgaatcctaagttttttggygaucttttaggtt	3002
Dp	57182	CATCAGCTGGAAPAAAGTTT-----AGGTT	57155
Qy	3003	ttccaaataataagatcatctgcnaacaagataattgactcttccttccaat	3062
Dp	57158	TCTTAAAAAANAAGAGTGAGGAGACATTCGCCATT-----	57119
Qy	3063	gfatgcacattcttccttcctctctgctgctatcataagagctccaglatatgttgaa	3122
Dp	57119	-----	57119
Qy	3123	aacagtgtaaaatgggcactctgtgtctgatacttcaggaagagccttagttct	3182
Dp	57119	--CAGGTGATGTTGGCTGTGGGTTTCAACATGGAATTAAGA-----	57077
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Dp	57077	--CATACCTCAGATTAATA-----ATATCTTCTTATTAATTCAGAGT	57038
Qy	3243	atgttcctctcatalacacagttttttggaaattttatcatgaaggaatgtaat	3302
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Qy	3303	caa-----cgtcttttcagatacaacgcgaatgataatagttttgtctcattctgt	3359
Dp	56975	CATATGCTGCATTAATCTGCATCTATTGAATATATCATGTGGGTTTGTATTAAAGTTCTG	56918
Qy	3360	agataagacatacacaagcgtttgatttgcatactgcacaacacccttcacccctggga	3419
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Qy	3420	taaatccacattgatacagaatgagatcctttaaataatgttgtgaaccacattgcta	3479
Dp	56855	TAAAGCTCTACTTGACAGTGTGGGCAAGCTTTTGTATCTGCTGCTAAATTCAGTTTGCCA	56798
Qy	3480	gfatctgtcaggaattttacataaatttcatacagaaacacgagccgtgacttct	3539
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Qy	3540	tttttgatgtaatttgcctgttttgcatacaggaataactgcctgtagaatgagt	3599
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Dp	56678	TAGGAGAGCGCTCCCTTCCTCAATTTTGGGAATATGTTTCAGTAGGAATGCTACTAGCT	56619
Qy	3658	-ttcttcaagctcttgtagaaattcagagtgaaataactccgggtccag-----	3706
Dp	56618	CTTCTTTGTACATCTGGTAGAATTCAGCATGAATATCATCTGTGCTTGCGCTTTTTCGG	56558
Qy	3706	-----actctgtaacttttataactcgttcagttt	3739
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Qy	3740	agattcttcaaggtcccaatattgtagagaaatgataatgtagataggaattataacttct	3799
Dp	56498	CAGTTTCTCTCGTTCAAGTCTTTGGAGGGATATGATGTGACATGAATTAATTCATTTCTT	56439
Qy	3800	ctagattttccaattatattgagcatataatattgctcatagtagccaacaaatgactcttgaa	3859
Dp	56438	GGAGATTTTCTAGTTTATTTCGATAGTGGTGTTCAATAATATCTTAATAGATGTTGTTGTA	56379
Qy	3860	tttctgatatcacagttgaaatgcctcccttcaatcttgatttattattatttaggtgc	3918
Dp	56378	TTTTTGTGGGGTCAGTGGCAATATCCCTTGTTGCTTGCTTGCTTATTTATGATC	56320

RESULT	7
LOCUS	AC006288 220218 bp DNA PRI 16-JAN-1999
DEFINITION	Homo sapiens chromosome 9, clone hRPK.295_D_22, complete sequence
ACCESSION	AC006288
VERSION	AC006288.1 GI:4160142
KEYWORDS	HTG.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euarchonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 220218) Birren,B., Linton,L., Nusbaum,C. and Lande,E. Homo sapiens chromosome 9, clone hRPK.295_D_22 Unpublished
JOURNAL	2 (bases 1 to 220218)
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lande,E., Allen,N., Anderson,M, Baker,J., Baldwin,J., Barna,N., Beckert,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collingore,A., Cooke,P., Dearrellano,K., Depayre,E., Devon,K., Dewar,K., Donelan,L., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagsos,B., Heaford,A., Herena,L., Horton,L., Howland,J.C., Jones,G., Kann,L., Karatas,A., Lenczky,J., MacDonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., Meldrum,J., Molla,M., Morris,W., Morrow,J., Mychalecky,J., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Testaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE	Direct Submission
JOURNAL	Submitted (05-JAN-1999) Whitehead Institute/MIT center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	3 (bases 1 to 220218)
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lande,E., Allen,N., Anderson,M, Baker,J., Baldwin,J., Barna,N., Beckert,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collingore,A., Cooke,P., Dearrellano,K., Depayre,E., Devon,K., Dewar,K., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G., Hagsos,B., Heaford,A., Horton,L., Howland,J.C., Jones,G., Kann,L., Karatas,A., Lenczky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J., Molla,M., Morris,W., Morrow,J., Mychalecky,J., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Testaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-JAN-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Jan 16, 1999 this sequence version replaced g1:4156127. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a> . location/Qualifiers
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Dh 60710 CAGAAATGGAAAAACCTACTTTAAAGTTCAATGGAACCAAAAAAGAGCCCGCATCGCA 60769  
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Dh 60770 AGTAATCTTAAGCCAAAGAAAGAGCTGGAGGATCATCTACTCTACCTCCCAACAT 60829  
Qy 301 actcaagagctgaagtaacaaacagatgtagtactgttaccaaaacgaataataagacc 360  
Dh 60830 ACTCAAGGCTTACAGTAACCAAAACGCATGTGTAATGTTACCAAAACAGAAATATAGTTC 60889  
Qy 361 aatgtagtgaacagatccctcagaaataataacacacatctacacacatctgactcttg 420  
Dh 60890 AATGGAACAGAAACAGAGCCCTCAGAAATACGCCGCATACACTACATATGTGATCTTG 60949  
Qy 421 acaaacctgaaaagaacaagaataagggaaaggattccctatttaataatggtgctgg 480  
Dh 60950 ACAAACTGAGAAAAAACAAAGCAATGGGGAAGGATCCCTATTAAATGATGCTGG 61009  
Qy 481 aaaaactgctagccatagtatgaaagctgaaactggaatccctcctcctcaccctatacaa 540  
Dh 61010 AAAAATGGCTAGCCATATGTGGAAGCTGAAACTGGATCCCTCCCTTACACTTATACAA 61069  
Qy 541 aaatttaactaagatggttaaaagacttaaaagttagaagcctaaacccaataaaacccctag 600  
Dh 61070 AAATCAATTCAGATGATTAAGATTAAAGTTAAAGTTAGACTTAAACCAATAAACCCCTAG 61129  
Qy 601 aag-aaacttggaataccatcactgactataggaatggtgcaaggactctgactgaa 659  
Dh 61130 AAGAAACCTTGGGATTCACATTCAGGACATAGGCATGGCAAGGACTTCAATGCTTAA 61189  
Qy 660 caccaaaagcaatggaacaaaacaaaattgcaacaaacagatcccaatttaactaaaga 719  
Dh 61190 CACCAAAAGCATAGGCAACAAAGCCCAAAATTCAGAAATGGATCTTAATTAACCTAAAGA 61249  
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Dh 61250 GCTTCTGCAGCAAAAGAACTACCATCAGAGTGAACAGGCAACCTCAAAATGGGAGA 61309  
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Dh 61429 AGACACTCTCAAAAAGAAAGATTTATGCACCAAAAAACATGAAAAAATGTCATCA 61488  
Qy 957 tcaactggccatcagagacatgcaaatcaaaccaaatgagataccatctcaaccagtt 1016  
Dh 61489 TCACCTGGCCATCAGAAATCAAAATCAAAACCATATGAGATACCATCTCACACCAAT 61548  
Qy 1017 agaatggaatcatttaaaagtcaagaaacaaacaggtgctggagaggtgtgtggagaata 1076  
Dh 61549 AGAATGGCAATCATTTAAAAATCAGGAACAACAGGTGCTGGAGGATGTGGAAAAATA 61608  
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Dh 61729 GGTATATACCCAAATGACTATTAATCATGCTGTATTAAGACACATGCAACGATGTGTT 61788

Qy 1257 atgtggcactatcacataagcaaaagacctbggaaccaaccaaatgttccatcagtgta 1316  
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Qy 1317 gactggaatgaagaatgtgtgcatgtatcacagtggaatatattgacccat-aaaaag 1375  
Dh 61849 GACTGGATTAAAGAAATGTGGACATATACACCAATGGAATATCTATGATCAATAAAAAT 61908  
Qy 1376 gatgattcaactgctctgttgaagacatggaagtgtggaacacatctcagcaaa 1435  
Dh 61909 GATGAGTTCACTGCTCTTGTATGGGACATGATGAATTTGGAATCATCATCTTCAGTAAA 61968  
Qy 1436 ctatcacagaagatagaanaaccaacacacacatgtctcactcatagtgvggaaltgaca 1495  
Dh 61969 CTATCGCAAGCAAAAAAACCAACACTGCATATTCACATCAGTAGTGGGAATTTGAACA 62028  
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COMMENT	Lloyd,D. Direct Submission Submitted (17-NOV-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humuquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 18, 1999 this sequence version replaced gi:6065948. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n s separate segments.		
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Q 1255 ttattgtgacatctcacaaatagcaagaactgtgaacccaacccaatgttccatcagttg 1314
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Q 1375 ggtatgttcaagctccttctgttaaggaacatgagaaagttgaaacatcttgcagaa 1434
D 16065 AGATGAGTTCATCTCTCTTTGTAGGACATGATGAAAGCTGGAAACCATCATTTGTGACAA 16124
Q 1435 actatacaagga tagaaaaaccaacaacacatglttcaactaatagtgtggaaattgaac 1494
D 16125 ACTATGCAAGGAAAGAAAAACCAACACACATGTTCTCACTAATAGTGGGGAATTAAGAC 16184
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Q 1555 ggggaagggggaaggaatagcattagaatatataccatgtaaaagtatgtaagtgt 1614
D 16245 GGGGAGGGGGGAGGGGTAGTATAGAGATATACCTAATGTAA---ATGAGTTAATGGGT 16301
Q 1615 gcaacataccaacatggaacatgataacaaacaaacacacacacacacacacacacac 1674
D 16302 GCAGACACCAACATGACATGATATACAT -ATGTAACAAACCTGACATTTGTACACATG 16360
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D 16361 TGTACACCTTAGAACCTTCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 16420
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AUTHORS	Stone,N.E., Keseler,I.M., Schmutz,J.J., Shang,J., Cox,D.R. and Myers,R.M.		
TITLE	Direct Submission		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 161326)		
AUTHORS	Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.		
JOURNAL	Direct Submission		
TITLE	Submitted (28-JAN-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA		
REFERENCE	3 (bases 1 to 161326)		
AUTHORS	Stone,N.E., Keseler,I.M., Schmutz,J.J., Shang,J., Cox,D.R. and Myers,R.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-NOV-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA		
COMMENT	On Nov 9, 1998 this sequence version replaced gi:3694642. Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.8		
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
3	Stone, N.E., Kessel, I.M., Schmutz, J.J., Shang, J., Cox, D.R. and Myers, R.M.	Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA (bases 1 to 110401)		
		Direct Submission		
		Submitted (10-APR-1998)	Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA	
		On Apr 17, 1998 this sequence version replaced gi:2914680.		

FEATURES	Location/Qualifiers
source	1. .110401

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QY	299	atactacaaggtctacagttaaccaaaacagcatggtactggtatccaaaaac--agaata	356
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OY	1193	actgggtatgtacccaagaagattataaalcacgtcgtcgtlaaagacacatgcacatgtat	1252
Db	87287	GCTGGGTATATACCCAAAGGATTATAATCATGCTGCTATAAAGACATGACAA--CAT	87230
OY	1253	gtttattgtgcacatattcacaatgtgcaaaagccttggaaaccaacccaatgtccatcagt	1312
Db	87229	GTTTATTGAGGCATTTTCACCATGTGCAAAAGACTTGGAAACCAACCAATATGCATCAAT	87170
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OY	1432	caaatcatcaagaagttaaaaaaccaaacaccacagtcttcatcacatagtgagggaatg	1491
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VERSION AL080275.8  
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Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Nickerson, J.  
TITLE Direct Submission  
JOURNLS Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquey@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Sep 12, 1999 this sequence version replaced gi:5823982.  
IMPORTANT: This sequence is unfinished and does not necessarily  
represent the correct sequence. Work on the sequence is in progress  
and the release of this data is based on the understanding that the  
sequence may change as work continues. The sequence may be  
contaminated with foreign sequence from E.coli, yeast, vector,  
phage etc. Order of segments is not known: 800 n's separate  
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NOTE: This is a 'working draft' sequence.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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ORIGIN

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FEATURES

Location/Qualifiers

[illegible]

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LOCUS	HS93L7		
DEFINITION	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21.		
	206784 bp	DNA	PRI
			23-NOV-1999

RESULT	14	
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LOCUS	HS93L7	206784 bp DNA
DEFINITION	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21.	PR1 23-NOV-1999

ACCESSION A022401.1 GI:3059060  
 VERSION HTG; CHM; Choroideraemia; geranylgeranyltransferase component A 1;  
 KEYWORDS RAB Escort; REP-1; REP1; Tapetochoroidal Dystrophy; TCD.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutharia; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 206784)  
 AUTHORS Grifham, D.  
 JOURNAL Direct Submission  
 Submitted (26-MAR-1998) Chromosome X Project Group  
 (http://www.sanger.ac.uk/HGP/ChrX/) Sanger Centre, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 IMPORTANT: This sequence is the entire insert of clone 93L7. During  
 sequence assembly data is compared from overlapping clones. Where  
 differences are found these are annotated as variations together  
 with a note of the overlapping clone name. Note that the variations  
 annotated may not be found in the sequence submission corresponding  
 to the overlapping clone as we submit sequences with only a small  
 overlap as described above.  
 This sequence was generated from part of bacterial clone contigs of  
 human chromosome X, constructed by the Sanger Centre chromosome X  
 mapping group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/ChrX/  
 This sequence has been finished according to sequence map criteria  
 as follows. An attempt is made to resolve all sequencing problems,  
 such as compressions and repeats, but not necessarily within known  
 annotated human repeat sequence elements (e.g. Alu). Where the  
 sequence is ambiguous, there is an annotation using the 'unsure'  
 feature key.  
 The true left end of clone 93L7 is at 1 in this sequence. The true  
 right end of clone dA43C13 is at 36921.  
 The true right end of clone 93L7 is at 206784.  
 93L7 is from the library RPCII constructed at the Roswell Park  
 Cancer Institute by the group of Pieter de Jong.  
 For further details see http://bacpac.med.buffalo.edu/  
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Best Local Similarity 78.8%; Pred. No. 5.4e-255;
Matches 2083; Conservative 0; Mismatches 441; Indels 120; Gaps 17;
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Db 961 GGCATCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020  
OY 961 ggcatacatgatttaatttaatttaatttaatttaatttaatttaatttaatttaatt 1020  
Db 1021 TTGGAGCCAGACATTTGAGTCTGCAACCTTTTACAGGCTCAAGAGTGTGCTTTCAA 1080  
OY 1021 ttggagccagacattttagctgcaaccttttacagagctcaagagtgtgctttcaa 1080  
Db 1081 TATGGGCGAGATAGTCTGCTGCCAAGAAATGCTGAGAGAGGCACTGAAGCTCTCAACG 1140  
OY 1081 tatggcgagatagctgctgccaaagaaatgctgagagaggcaactgaagctctcaacg 1140  
Db 1141 AATCTTCCCTTACAACTTAATCTCTGTTTCTGCATATCCATGAGTGAAGAAACAGACA 1200  
OY 1141 aatcttcccttaacaacttaattctctgtttctgcataccatgtagaagaaacagaca 1200  
Db 1201 CTTTCATTAATGTAATCGGACGCCAAGAGACCACCTCCAGGAGAAAGAGCTGGC 1260  
OY 1201 ctttcatttaagttaacggaagcccaagagcccaactccaggaagaaagagctggc 1260  
Db 1261 ACAACTTACCGGCAAACTGTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
OY 1261 acaacttacccggcaaaactgtgctgcttctgctgctgctgctgctgctgctgctgct 1320  
Db 1321 TCTTTTCACTGCAAGTATTAATGAGCACTGAGTATGATGAGTATGATGAGTATGATG 1380  
OY 1321 tcttttcactgcaagtatttaattgagcaactgagatgagatgagatgagatgagatgag 1380  
Db 1381 GGAAGCTCAAAATTTGTTTCAGATCATTAAGGCTTACTAGACTTTGCTATACACCA 1440  
OY 1381 ggaagctcaaaatfttctcagatcattaaagcttaactagactatctgcatacacca 1440  
Db 1441 CCGGCTGGCTCAAAAGGCTGTGTTCAATATTAATTAATTAATTAATTAATTAATTA 1500  
OY 1441 ccggctggctcaaaaggctgtgttcaaatatttaatttaatttaatttaatttaattta 1500

Db 1501 CAACCTCCCCCTGAAGGCGAGGCAATTGAATCGTGCAATGCTGCTGAGACACTGAT 1560  
OY |||||  
OY 1501 caacctccccctgaaaggcgagggcatltgaatcgtggtacatcggtgctgagacactggt 1560  
Db 1561 CTTCAACAAGCTCATATGAGGACACCTGGAATTTGGCCATGAGTAAAGCTCCGAGCCT 1620  
OY 1561 ctccaagaactcataatgagacactggaatttggcattgagttagctcccgagccct 1620  
Db 1621 TCAGATGTGGGCACTGCTCCAGATCCCAACGACATTTATCAGTCCCTCTGCAAGACTTG 1680  
OY 1621 tcagatgtgggcactgctccaagatcccaacgacatttaccgtccctctgcaagacttg 1680  
Db 1681 CAGATGCTCTCTCTGAACGAGATACCGGCAATTTGATTCAGAGTCTGGGCGGCTGTG 1740  
OY 1681 cagatgctctctctgaacgagataccggcaatttgatccagagtgctggcggtgtg 1740  
Db 1741 GGAAGCTTCTGTAACACAGGACACATCTTCAGCAAGGCAATTTTCTAATTTGTCTGCTT 1800  
OY 1741 ggaagcttctgtaaacagagacaacatcttcagcaaggcaatttctattttgtcgtct 1800  
Db 1801 GGAATCTGCTTATTTCTGCTTTTATTAATGACATTTGAAGAAATGTTGGAATCTAT 1860  
OY 1801 ggaatctgcttattctgttttatttaagaacattgaaagaaatgtttggaattcat 1860  
Db 1861 ACACCAATAGAAACACAGAACATCCGCAAGTCCACAGTGGAGCTCTCGGCACTTGA 1920  
OY 1861 acaccaatagaaaacagaaaccccaagttcccaagtgagctcctcctggaattta 1920  
Db 1921 TTCCTGTAGCTATCTGAGAGTGTGAAGCAGGGGTAGGCAAGACATACACTTCAG 1980  
OY 1921 ttcctgtagctatctgagagtgtagagcagggtaggcaagacatacacttcag 1980  
Db 1981 AGACCCAGGATGCGACACTTCAGGAATGGACACTTTTACAAATTTTCCATTAAGCT 2040  
OY 1981 agaccagatgctgcagacttcaggaatggacacttttacaattttccaataagct 2040  
Db 2041 AAAAATCTTTTGGCAAGAAACCATGACACTACTACTATGAGGAATATATAGGTAC 2100  
OY 2041 aaaaatcttttggcaagaaaccatgacactactactactactactactactactactact 2100  
Db 2101 ATGGAGGGGCAAGTCTTCTCACTTCAAAAACAAATCAAAAGACAGTCAAGAAATGCCAA 2160  
OY 2101 atggaggggcaagtcttctcacttcaaaaacaaatcaaaagacagtcgaagaaatgccaa 2160  
Db 2161 GCCAGTGGGAGAGTACTCAAGAACTTGAGAAATGCTGCTGCTCAAAATACCACTGGC 2220  
OY 2161 gccagtgggagagactcaacaaagacttgagaatctgtgtgtctcaaaatacacactggc 2220  
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OY 2221 ctgtcttttggcccaaggcttaccacactgattgacttacttacttacttacttacttact 2280  
Db 2281 GGGGAGAAATGTGGCTCTTCTGAACACAGCCTTGCGGCTCTGAAACACAGGGGAT 2340  
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Db 2521 GACATCATTTCTAATGATGTAAGAAAAAAGATTTAATTAAGCACT 2567  
OY 2521 gacatcatcttctaataatgtaagaaaaaagattttaataagcact 2567



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